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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 09:49:12 ; Search time 9268.38 Seconds
(without alignments)
11250.684 Million cell updates/sec

Title: US-09-841-894A-16

Perfect score: 2152

Sequence: 1 GGGGCTGTACCGAGGGGTGC.....AAGGCTTCTTATATGTTA 2152

Scoring table: 'OLIGO_NUC', Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2152	100.0	2152	AR112295
2	2150	99.9	3306	9 BC050416
3	2088	97.0	2904	6 AR278710
4	2088	97.0	2904	6 AR400442
5	2088	97.0	2904	6 AR405709
6	2088	97.0	2904	6 AR564089
7	2088	97.0	2904	6 AX200994
8	2088	97.0	2904	6 AX267729
9	2029	94.3	3320	6 AX327336
10	1972	91.6	2143	6 AR112294
11	1968	91.4	4034	6 AR278711
12	1968	91.4	4034	6 AR400443
13	1968	91.4	4034	6 AR405710
14	1968	91.4	4034	6 AR564090
15	1968	91.4	4034	6 AX200995
16	1968	91.4	4034	6 AX267730
17	1936	90.0	4894	6 AR278709
18	1936	90.0	4894	6 AR400441
19	1936	90.0	4894	6 AR405708

ALIGNMENTS

Result 1	AR112295	AR112295	AR112295	AR112295.1	GT:14092195
LOCUS	AR112295	AR112295	AR112295	AR112295.1	GT:14092195
DEFINITION	Sequence	16	from patent	US 6130043.	
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					

REFERENCE	AUTHORS	JOURNAL	TITLE	FEATURES	SOURCE
1 (bases 1 to 2152)	Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hedges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.		Reagents and methods useful for detecting diseases of the prostate	Patent: US 6130043-A 16 10-OCT-2000; Location/Qualifiers	1. .2152

ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
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	Mismatches	Pred. No.	0;		
	0;	Mismatches	0;	Indels	0;
				Gaps	0;

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QY	121	CTCTCTGGTCATGGACCGGACTCGAGCTTCTGAGTGGCCATCTCCCTGGCTT	180
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QY	181	TGTGGCAGCTTCCCTGTGGCTGCCAACATGCCCTGCCCCAACATGCCCTGCCCCGGT	240
Db	181	TGTGGCAGCTTCCCTGTGGCTGCCAACATGCCCTGCCCCAACATGCCCTGCCCCGGT	240

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Qy	961	CTCCCCACTCTAGGGCTGCCTGACTGGGCTTCCAAAGGGGTTTCAGTCGGACTT	1020	Db	3181	TTTGCATAATGTCGTCATTATTAGGGGGTGAATTATACTGTAAGTGAGCA	3240
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Qy	1021	ATACAGGGAGGCCAGAAGGGCTCCATGCACTGGATGCGGGACTCTGCAGGTGATTAC	1080	Db	3241	ATCAGAGTATAATGTTATGGTACAAATAAGGCTTTCTTATATGT	3290
Db	2161	ATACAGGGAGGCCAGAAGGGCTCCATGCACTGGATGCGGGACTCTGCAGGTGATTAC	2220	Qy	1081	CGAGGCTCAGGGTTAACAGCTAGCCCTTAGTGTAGACACACACTAGAGAAGGGTTTG	1140
Db	2221	CGAGGCTCAGGGTTAACAGCTAGCCCTCTAGTTGAGACACACACTAGAGAAGGGTTTG	2280	Db	2281	GAGCTGAATAACTCACTGACACCTGGTTCCATCTAACGGCTTAACTGGAGCTCG	1200
Qy	1141	GAGCTGAATAACTCACTGACACCTGGTTCCATCTAACGGCTTAACTGGAGCTCG	1200	Qy	1201	TTAATGTTGACTCTGCATGGGAGTTCTAGGATGAAACACTCCATGGGATTGAAC	1260
Db	2401	TTAATGTTGACTCTGCATGGGAGTTCTAGGATGAAACACTCCATGGGATTGAAC	1260	Db	2341	TTAATGTTGACTCTGCATGGGAGTTCTAGGATGAAACACTCCATGGGATTGAAC	2400
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Db	2461	ATATGAAAGTTATTGTTAGGGGAGAGTCTCTAGGGGAAACACACAGAGGTTCCC	2460	Qy	1321	TCAGCCCACAGCACTGCTTTGCTGATCCACCCCTCTACCTTTACAGGATG	1380
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Qy	1381	GCTGTGGTCTCTGTGCCATCACAGAGACACAGGATTAATTAACCTATT	1440	Db	2521	GCTGTGGTCTCTGTGCCATCACAGAGACACAGGATTAATTAACCTATT	2580
Db	2521	GCTGTGGTCTCTGTGCCATCACAGAGACACAGGATTAATTAACCTATT	2580	Qy	1441	ATTAACAAAGTAGAACGGATCCATTGCTAGCTTCTGTGTTGTTAATATTG	1500
Db	2581	ATTAACAAAGTAGAACGGATCCATTGCTAGCTTCTGTGTTGTTAATATTG	1500	Db	2581	ATTAACAAAGTAGAACGGATCCATTGCTAGCTTCTGTGTTGTTAATATTG	2640
Qy	1501	GTAGGGTGGGGATCCCAAACATCAGGCCCCCTGAGATAGCTGGCATGGGTGATCA	1560	Db	2641	GTAGGGTGGGGATCCCAAACATCAGGCCCCCTGAGATAGCTGGCATGGGTGATCA	2700
Db	2641	GTAGGGTGGGGATCCCAAACATCAGGCCCCCTGAGATAGCTGGCATGGGTGATCA	2700	Qy	1561	TTGCCAGAAATCTCTCTCTGGGGCTCTGGCCCCAAATGCTAACCCAGGCTTG	1620
Db	2701	TTGCCAGAAATCTCTCTCTGGGGCTCTGGCCCCAAATGCTAACCCAGGCTTG	1620	Db	2701	TTGCCAGAAATCTCTCTCTGGGGCTCTGGCCCCAAATGCTAACCCAGGCTTG	2760
Qy	1621	AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTACCAAGGTTAGGGTGTGAA	1680	Db	2761	AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTACCAAGGTTAGGGTGTGAA	2820
Db	2761	AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTACCAAGGTTAGGGTGTGAA	2820	Qy	1681	GGAAGGTAGAGGGTGGGGCTCAGCTCAACGGCTCCCTAACCCCTCTCTTG	1740
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Db	2881	GCCCCAGCTGTCCCCCACTTCCACTCCCTCTACTCTCTAGGACTGGGCTGTGAA	2880	Qy	1801	AGGCACTGCCCCAAATTCCCTACCCCAACTTTCCACTTCCACTCCCTCTAGGACTGGGCTGTGAA	2940
Qy	1801	AGGCACTGCCCCAAATTCCCTACCCCAACTTTCCACTTCCACTCCCTCTAGGACTGGGCTGTGAA	2940	Db	2941	AGGCACTGCCCCAAATTCCCTACCCCAACTTTCCACTCCCTCTAGGACTGGGCTGTGAA	3000
Db	2941	AGGCACTGCCCCAAATTCCCTACCCCAACTTTCCACTCCCTCTAGGACTGGGCTGTGAA	3000	Qy	1861	GCTCCACAACCCCTGTGGAGCTACTGCACTTCCCTACCCCAACTTTCCCAAG	1920
Qy	1921	CCTTGTCCATCTCAGCCCCCAGAGTATCTGTGTTGGGAATCTCACACAGAACTC	1920	Db	3001	GCTCCACAACCCCTGTGGAGCTACTGCACTTCCCTACCCCAACTTTCCCAAG	3060
Db	3001	GCTCCACAACCCCTGTGGAGCTACTGCACTTCCCTACCCCAACTTTCCCAAG	3060	Qy	1920	GCTCCACAACCCCTGTGGAGCTACTGCACTTCCCTACCCCAACTTTCCCAAG	1860
Qy	1920	GCTCCACAACCCCTGTGGAGCTACTGCACTTCCCTACCCCAACTTTCCCAAG	1860	Db	3061	CCTTGTCCATCTCAGCCCCCAGAGTATCTGTGTTGGGAATCTCACACAGAACTC	3120
Qy	1981	AGGAGCACCCCTGCCTAGCTAAGGGAGCTTATCTCTAGGGGGTTAAGTGCCG	2040	Db	3121	AGGAGCACCCCTGCCTAGCTAAGGGAGCTTATCTCTAGGGGGTTAAGTGCCG	3180
Db	3121	AGGAGCACCCCTGCCTAGCTAAGGGAGCTTATCTCTAGGGGGTTAAGTGCCG	3180	Qy	545	GCCAGGGTTCGGGGGCATCTGGGACCTCGCCATCTGGGAGCTCGCCATCTGGGAGCTCGCC	1352
Db	3121	AGGAGCACCCCTGCCTAGCTAAGGGAGCTTATCTCTAGGGGGTTAAGTGCCG	3180	Qy	545	GCCAGGGTTCGGGGGCATCTGGGACCTCGCCATCTGGGAGCTCGCCATCTGGGAGCTCGCC	1352

Qy	605	CAGCTGTCCCAGGTGGCCCCATCCCTTATGGCTCATGGTCAGCAGTCT	664	Qy	1685	GGTAGAGGGTGGGGCTTCAGGCTCAACGGCTCCAAACCCCTCTCTGGCC	1744
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Qy	665	GTCACTGCCTATATGGTGTCTGCCAGGCCCTGGCTGGCTGCCATTACTTGCTACA	724	Qy	1745	AGCCTGGTCCCCCACTTCACTCCCTACTCTCTCTAGGACTGGGCTGATGAGGC	1804
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Qy	725	CAGGTAGTATTGACAAGAGGGACTTGCCAAATACTCAGCGTAGAAACTCCAGCACA	784	Qy	1805	ACTGCCAATAATTCCCCTACCCCAACTTCCCCTACCCCAACTTCCCACAGCCTC	1864
Db	1473	CAGGTAGTATTGACAAGAGGGACTTGCCAAATACTCAGCGTAGAAACTCCAGCACA	1532	Db	2553	ACTGCCAATAATTCCCCTACCCCAACTTCCCCTACCCCAACTTCCCACAGCCTC	2612
Qy	785	TTCGGGTGGAGGGCTGCCCTGACTGGTCCAGCTCCCCTCTGTAGGCCATGGGG	844	Qy	1865	CACACCCCTGGAGCTACTGCAGGACAGACAAGTGGGTTCCAAAGGCC	1924
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Db	1833	GCTCAGGGTAAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAACGGGTTGGGAGC	1892				
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Qy	1385	GTTGGTCTCTGTCATCACAGAGCACAGGGCATTAATTAATTTAATTTATTT	1444				
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Query Match 97.0%; Score 2088; DB 6; Length 2904;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
 Kalos, M.D., Fanger, G.R., Rettner, M.W., Stolk, J.A., Day, C.H.,
 Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
 Hepler, W.T. and Henderson, R.A.
 KEYWORDS Compositions and methods for the therapy and diagnosis of prostate
 SOURCE Unknown.
 ORGANISM Unclassified.

1 (bases 1 to 2904)

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6620922-A 703 16-SEP-2003;
 FEATURES Location/Qualifiers 1. . 2904
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 /mol_type="genomic DNA"

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RESULT 5 AR405709							
LOCUS	AR405709	2904 bp	DNA	linear	PAT 18-DEC-2003		
DEFINITION	Sequence 703 from patent US 6630305.						
ACCESSION	AR405709						
VERSION	AR405709.1	GI:40154546					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 2904)						
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.						
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer						

JOURNAL	Patent:	US 6630305-A 703 07-OCT-2003;	Db	1713 CCAGTCTCTAGGGCTGCCTGACTGGAGGCCTCCAGGGGTTCAAGTCTGGACTTATAC 1772
FEATURES	Location/Qualifiers		Qy	1025 AGGGAGCCAGAAGGGCTCCATGCACTGGATGCCGGACTCTGCAGGGATTACCCAG 1084
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Query	Match 97.0%; Score 2088; DB 6; Length 2904;		Db	1833 GCTCAAGGGTTAACAGCTAGGCCTCTAGTGAGACACACCTAGAGAAGGGTTGGGAGC 1892
Best	Local Similarity 100.0%; Pred. No. 0;	Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1145 TGAATAACTCACTCACCTGGTTCCATCTTAAGCCCTTAACCTGAGCTTGGTTA 1204
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Qy	305 GCCTCCCTACACACCGGGAGAACAGGAGCTTCTGCCAAATACGGAGGGACACTGGA 364		Qy	1385 GTGGTCTCTGTGCTGCATCACAGAACAGGACACAGGATTAATTTAATTACTT 1444
Db	1053 GCTCCCTCACACCGGGAGAACAGGAGCTTCTGCAGGCTTCTGGCTTACACACTG 1112		Db	2113 GTGGTCTCTGTGCTGCATCACAGAACAGGACACAGGATTAATTTAATTACTT 2192
Qy	365 GGTGCTAGCACTGGAGAACAGCCTGTATGACCAGCTTCTGGCTTACACACTG 424		Qy	1445 AACAAAGTAGAGGAATTCATGGGAGCT 1504
Db	1113 GGTGCTAGCACTGGAGAACAGGAGCTTCTGGCTTACACACTG 1172		Db	2193 AACAAAGTAGAGGAATTCATGGGAGCT 2252
Qy	425 CCCTCCCTAATGGACACGTGGTCTGGAGGCACTGGCTTACCTCCACCCGG 484		Qy	1505 GGTGGGGATCCCCAACATCAGGTCCCCTGAGATAGCTGGCATGGCTATTC 1564
Db	1173 CCCTCCCTAATGGACACGTGGTCTGGAGGCACTGGCTTACCTCCACCCGG 1232		Db	2253 GGTGGGGATCCCCAACATCAGGTCCCCTGAGATAGCTGGCATGGCTATTC 2312
Qy	545 GCCAGGGTTCGGGGCCATCTGCTGGACTCGCCATTCGGATAGTGCTTC 604		Qy	1565 CAGAATCTCTCTGGGCTGGCCCCAAATGCCAACGGACCTGGAAAT 1624
Db	1233 CTCTGGGGGCTCTGCTGGTCTCCGGGGGATCTGCCATCTGGATAGTGCTTC 1352		Db	2313 CAGAATCTCTCTGGGCTGGGCTCTGGGGGATCTGCCATCTGGATAGTGCTTC 2372
Qy	605 CTGCTGCCCCAGGTGGCCCATCCCTGTTATGGCTCATGGCTCAGCAGCT 664		Qy	1625 TCTACTCATCCCAATGATAATTCCAATGCCAACGGTTAGGGTGTGAAGGA 1684
Db	1353 CTGCTGCCCCAGGTGGCCCATCCCTGTTATGGCTCAGCAGCT 1412		Db	2373 TCTACTCATCCCAATGATAATTCCAATGCCAACGGTTAGGGTGTGAAGGA 2432
Qy	665 GTCACTGCCTATATGGTGTCTGCCAGGCCACTGGCTTACCCCTCTGGCC 1412		Qy	1685 GGTAGAGGGGGCTCAGGTCTCACGGCTTACCCACCCCTCTGGCC 1744
Db	1413 GTCACTGCCTATATGGTGTCTGCCAGGCCACTGGCTTACCCCTCTGGCC 1352		Db	2433 GGTAGAGGGGGCTCAGGTCTCACGGCTTACCCACCCCTCTGGCC 2492
Qy	725 CAGGTAGTATTGACAAGAGGCACTGGCTTACCCCAACTCGGTAGAAACTCCACCA 724		Qy	1745 AGCCTGGTCCCCCACTTCACTCCCTACTCTCTCTAGGACTGGCTGATGAGGC 1804
Db	1473 CAGGTAGTATTGACAAGAGGCACTGGCTTACCCCAACTCGGTAGAAACTCCACCA 1472		Db	2493 AGCCTGGTCCCCCACTTCACTCCCTACTCTCTAGGACTGGCTGATGAGGC 2552
Qy	785 TGGGGTGGAGGGCCTGCCACTGGCTTACCCCAACTCGGTAGAAACTCCACCA 784		Qy	1805 ACTGCCAACATTCCCTACCCCAACTTCCCTACCCCAACTTCCCACTGGCTGATGAGGC 1864
Db	1533 TGGGGTGGAGGGCCTGCCACTGGCTTACCCCAACTCGGTAGAAACTCCACCA 1532		Db	2553 ACTGCCAACATTCCCTACCCCAACTTCCCTACTCTCTAGGACTGGCTGATGAGGC 2612
Qy	845 CTGGCGGGCTGCCAGTTCTGGCTTACCCCAACTCGGTAGAAACTCCACCA 1592		Qy	1865 CACAAACCTGGTACTGGAGCTACTGCCAACAGGACACAAAGTGGGTTCCAAGGCT 1924
Db	1593 CTGGCGGGCTGCCAGTTCTGGCTTACCCCAACTCGGTAGAAACTCCACCA 1652		Db	2613 CACAAACCTGGTACTGGAGCTACTGCCAACAGGACACAAAGTGGGTTCCAAGGCT 2672
Qy	905 CTGGCTGCTGAGGTGGTAGCTGCACAGCTGGGGCTCTGCTGCCAC 964		Qy	1925 GCACCCCTGCTGAGCTATCTCAGGGGGTTAAGTGGCTTCTGCTGCCAC 1984
Db	1653 CTGGCTGCTGAGGTGGTAGCTGCACAGCTGGGGCTGGCTCTGCTGCCAC 1712		Db	2673 TGTCCATCTCAGCCCCAGGATATCTGCTGCTGGGGTTAAGTGGCTTCTGCTGCCAC 2792
Qy	965 CCAGTCTCTGGCTGAGGTGGTAGCTGCACAGCTGGGGCTGGGGCTCTGCTGCCAC 1024		Qy	2045 CAATAATGTCCTATTAGTCAGGGGTGAAATTATCTCAGACAGCTAGTCAGCACTCA 2104
Db	2793 CAATAATGTCCTATTAGTCAGGGGTGAAATTATCTCAGACAGCTAGTCAGCACTCA 2852		Db	2793 CAATAATGTCCTATTAGTCAGGGGTGAAATTATCTCAGACAGCTAGTCAGCACTCA 2852

QY	2105	GAGTATAATGTTTATGGGACAAATTAAAGGCTTCTTATATGTTA	2152
Db	2853	GAGTATAATGTTTATGGGACAAATTAAAGGCTTCTTATATGTTA	2900
QY	665	GTCACTGCCTATATGGTCTGGCCAGGCCATTACTCAGGTAGAAACTTCAGCACA	724
Db	1413	GTCACTGCCTATATGGTCTGGCCAGGCCATTACTCAGGTAGAAACTTCAGCACA	1472
QY	725	CAGGTAGTATTGACAAAGAGGACTTGCCAATACTCAGGTAGAAACTTCAGCACA	784
Db	1473	CAGGTAGTATTGACAAAGAGGACTTGCCAATACTCAGGTAGAAACTTCAGCACA	1532
QY	785	TRGGGGTGGAGGGCTGCTACTGGTCCAGCTCCGCTCGTAGAAGACTTCAGCACA	844
Db	1533	TRGGGGTGGAGGGCTGCTACTGGTCCAGCTCCGCTCGTAGAAGACTTCAGCACA	1592
QY	845	CTGCCGGGTGGCCAGTTCTGTTCTGCAAAGTAATGGCTCTGCTGCCACC	904
Db	1593	CTGCCGGGTGGCCAGTTCTGTTCTGTTCTGCAAAGTAATGGCTCTGCTGCCACC	1652
QY	905	CTGTGCTCTGAGGTGCGTAGTGACACAGCTGGGCTGGGCTCCCTCCCTCC	964
Db	1653	CTGTGCTCTGAGGTGCGTAGTGACACAGCTGGGCTGGGCTCCCTCCCTCC	1712
QY	965	CCAGTCTCTAGGCTGCCACTGGGAATGGGCTTCAAGGGGACTCTGCAGGGATTACCA	1024
Db	1713	CCAGTCTCTAGGCTGCCACTGGGAATGGGCTTCAAGGGGACTCTGCAGGGATTACCA	1772
QY	1025	ACGGAGGCCAGAAGGGCTCCATGCCACTGGGAATGGGCTTCAAGGGGACTCTGCAGGGATTACCA	1084
Db	1773	ACGGAGGCCAGAAGGGCTCCATGCCACTGGGAATGGGCTTCAAGGGGACTCTGCAGGGATTACCA	1832
QY	1085	GCTCAGGGTTAACAGCTAGCCCTAGTTGAGACACACCTAGAGAAGGGTTGGAGC	1144
Db	1833	GCTCAGGGTTAACAGCTAGCCCTAGTTGAGACACACCTAGAGAAGGGTTGGAGC	1892
QY	1145	TGAATAAACCTCAGTCACCTGGTCCATCTCTAAGCCCTAACCTGCAGCTCGTTA	1204
Db	1893	TGAATAAACCTCAGTCACCTGGTCCATCTCTAAGCCCTAACCTGCAGCTCGTTA	1952
QY	1205	ATGTTAGCTCTGCATGGAGTTCTAGGATGAAACACTCTCCATGGGATTGACATAT	1264
Db	1953	ATGTTAGCTCTGCATGGAGTTCTAGGATGAAACACTCTCCATGGGATTGACATAT	2012
QY	1265	GAAAGTTATGGTAGGGAAAGGTCTCTGATCCACACACACAGCTGGGTTGGAGC	1324
Db	2013	GAAAGTTATGGTAGGGAAAGGTCTCTGATCCACACACAGCTGGGTTGGAGC	2072
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Db	2073	CCACACGACTGTCTTGTGATCCACACACAGCTGGGTTGGAGC	2132
QY	1385	GTGGTCTCTGTGATCCACACACACAGCTGGGTTGGAGC	1444
Db	2133	GTGGTCTCTGTGATCCACACACAGCTGGGTTGGAGC	2192
QY	1445	AACAAAGTAAAGGAATCCATGCTAGGAGCTTACGGTGTAAATTGGTAG	1504
Db	2193	AACAAAGTAAAGGAATCCATGCTAGGAGCTTACGGTGTAAATTGGTAG	2252
QY	1505	GGTGGGGATCCCCAACAACTCAGTCCCCCTGAGATAGCTGGTGTAAATTGGTAG	1564
Db	2253	GGTGGGGATCCCCAACAACTCAGTCCCCCTGAGATAGCTGGTGTAAATTGGTAG	2312
QY	1565	CAGAATCTCTCTGGTGTGATCTGGCTACGGTGTGGTGTAAATTGGTAG	1624
Db	2313	CAGAATCTCTCTGGTGTGATCTGGCTACGGTGTGGTGTAAATTGGTAG	2372
QY	1625	TCTACTCATCCAAATGATAATTCCAATGCTGTGTTAGGGTGTAAATTGGTAG	1684
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QY	1685	GTTAGAGGGTGGGCTCAGGTCTCAACGGCTCCCTAACCAAGGGTTAGGGTGTAAAGGAA	1744
Db	2433	GTTAGAGGGTGGGCTCAGGTCTCAACGGCTCCCTAACCAAGGGTTAGGGTGTAAAGGAA	2492

Qy	1745 AGCCTGGTCCCCCACTTCCACTCCCTACTCTCTAGGACTGGGTGATGAGGC	1804	Db	993 GCTTCAGCGCCCTCACCGGTTCACCTCTCAGCCCTGCAGATCCTGCCCTACACACTG	1052
Db	2493 AGCCTGGTCCCCCACTTCCACTCCCTACTCTCTAGGACTGGGTGATGAGGC	2552	Qy	305 GCCTCCCTACCAACCGGGAGAACGAGGGTTCTGCCCCAAATACCGAGGGACACTCGGA	364
Qy	1805 ACTGGCCAAATTCCCTACCCCACTTCCCTACCCCAACTTCCCACAGCTC	1864	Db	1053 GCCTCCCTACCAACCGGGAGAACGAGGGTTCTGCCAACATACGGAGGGACACTCGGA	1112
Db	2553 ACTGGCCAAATTCCCTACCCCAACTTCCCCTACCCCAACTTCCCACAGCTC	2612	Qy	365 GGTGCTAGGAGGACAGCCTGATGACCAGCTCCTGCCAGGCCAACGCTGAGCT	424
Qy	1865 CACAACCTGTTGGAGCTACTGCAGGACAGAACAGCTGCGGTTCCAAAGCCT	1924	Db	1113 GGTGCTAGGAGGACAGCCTGATGACCAGCTCCTGCCAGGCCAACGCTGAGCT	1172
Db	2613 CACAACCTGTTGGAGCTACTGCAGGACAGAACAGCTGCGGTTCCAAAGCCT	2672	Qy	425 CCCTCCCTAATGGACACGTGGGAGGCAAGGCACAAAGTGGGTTCCAAAGCCT	484
Qy	1925 TGTCCATCTCAGCCCCAGAGTATCTGTGCTTGGGAATCTCACAGAACAGGA	1984	Db	1173 CCCTTCCTAATGGACACGTGGGAGGCAAGGCACCTCCACCCCGG	1232
Db	2673 TGTCCATCTCAGCCCCAGAGTATCTGTGCTTGGGAATCTCACAGAACAGGA	2732	Qy	485 CTCTGGGGGCTCTGCTGTGATGTCCTCGCTAGTGTGGTGGGGTGGCCACCGAG	544
Qy	1985 GCACCCCTGCCGTGAGCTAAGGGAGGTATCTGTGCTTGGGAATCTCACAGAACAGGA	2104	Db	1293 GCCACGGGCTCTGCCTGTGATGTCCTCGCTAGTGTGGTGGGGTGGCCACCGAG	1292
Db	2733 GCACCCCTGCCGTGAGCTAAGGGAGGTATCTGTGCTTGGGAATCTCACAGAACAGGA	2792	Qy	545 CTGCTGCCCCAGGTGGCTGACCTCGCCATCTGGCTCCATGTCCAGCTAGCCACCGAG	604
Qy	2105 GAGTATAATGTTTATGGTACAAMATAAGGTTCTTATATGTTA	2152	Db	605 CTGCTGCCCCAGGTGGCTGACCTCGCCATCTGGCTCCATGTCCAGCTAGCCACCGAG	664
Db	2853 GAGTATAATGTTTATGGTACAAMATAAGGTTCTTATATGTTA	2900	Qy	1353 CTGCTGCCCCAGGTGGCTGACCTCGCCATCTGGCTCCATGTCCAGCTAGCCACCGAG	1412
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AX200994	AX200994 Sequence 624 from Patent WO0151633.	2904 bp DNA linear PAT 29-AUG-2001	Db	725 CAGGTAGTTGACAAGAGGACTGGCAAATACTCAGCTGAGAACACTCCAGCACA	784
LOCUS	DEFINITION		Db	1473 CAGGTAGTTGACAAGAGGACTGGCAAATACTCAGCTGAGAACACTCCAGCACA	1532
ACCESSION	VERSION	AX200994 AX200994.1 GI:15390821	Qy	785 TTGGGGTGGAGGGCTGCCTCACTGGTCCAGCTCCCGCTCTGTAGCCCCATGGGG	844
KEYWORDS	ORGANISM	Homo sapiens (human)	Db	1533 TTGGGGTGGAGGGCTGCCTCACTGGTCCAGCTCCCGCTCTGTAGCCCCATGGGG	1592
REFERENCE	AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.	Qy	845 CTGCGGGCTGCCAGTTCTGTGCTGCCAAAGTAATGGCTCTGTGCGACC	904
TITLE	JOURNAL	Compositions and methods for the therapy and diagnosis of prostate cancer	Db	1593 CTGCGGGCTGCCAGTTCTGTGCTGCCAAAGTAATGGCTCTGTGCGACC	1652
JOURNAL	CORIXA CORPORATION (US)	Patent: WO 0151633-A 624 19-JUL-2001;	Qy	905 CTGCGGTCTGAGGTGGCTAGCTGACAGCTGGGCTGGCTCTCTCTCC	964
FEATURES	source	Location/Qualifiers	Db	1653 CTGCGGTCTGAGGTGGCTAGCTGACAGCTGGGCTGGCTCTCTCTCC	1712
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ORIGIN					
Query Match 97.0%; Score 2088; DB 6; Length 2904;					
Best Local Similarity 100.0%; Pred. No. 0; Matches 2088; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 65 GCGGTTGGATGGGCAGGCTGGGGCTGTTCTGCACTGGCCATCTCCCTGGCTCTCT 124					
Db 813 GCGGTTGGATGGGCAGGCTGGGGCTGTTCTGCACTGGCCATCTCCCTGGCTCTCT 872					
Qy 125 CTGGTCATGGACCGGCTGGTCAGGGATTCGGCACTCGAGCAGTCTGGCTTAC 184					
Db 873 CTGGTCATGGACCGGCTGGTCAGGGATTCGGCACTCGAGTGGGACTCTGGAGTTACCCAG 1832					
Qy 1085 GCTCAGGGTAAACAGCTAGGCTCTAGTGTAGACACACCTAGAGAAGGGTTGGGAGC 1144					
Db 1833 GCTCAGGGTAAACAGCTAGGCTCTAGTGTAGACACACCTAGAGAAGGGTTGGGAGC 1892					
Qy 1145 TGAATAACTCACTCACCTGGTTCCATCTCTAACCCCTTAACCTCGAGCTTCGTTA 1204					
Db 1893 TGAATAACTCACTCACCTGGTTCCATCTCTAACCCCTTAACCTCGAGCTTCGTTA 1952					
Qy 1205 ATGTAAGCTCTCATGGAGTTCTAGGATGAAACACTCCTCCATGGGATTGAAACATAT 1264					
Db 1953 ATGTAAGCTCTCATGGAGTTCTAGGATGAAACACTCCTCCATGGGATTGAAACATAT 2012					
Qy 1265 GAAGTTATGAGGGAGAGTCTGAGGACACACCTAGAGAAGGGTTGGGAGC 1324					
Db 2013 GAAGTTATGAGGGAGAGTCTGAGGACACACCAAGAACAGGTTCCAG 2072					
Qy 245 GCTTCAGCGCCCTCACCGGGTCACCTCTGAGATCCTGCCCTACACACTG 304					
Db 2073 CCCACAGCACTCTTTGCTGATCCACCCCTTACCTTACAGGATGTTGCGCT 2132					

SOURCE	ORGANISM	Unknown.
REFERENCE	Unclassified	
	1 (bases 1 to 4034)	
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Repler, W.T. and Henderson, R.A.	
TITLE	Cancer Compositions and methods for the therapy and diagnosis of prostate	
JOURNAL	Patent: US 6512094-A 704 28-JAN-2003;	
FEATURES	Location/Qualifiers	
Source	1. . 4034 /organism="unknown" /mol_type="genomic DNA"	
ORIGIN		
Query	Query Match	91.4%; Score 1968; DB 6; Length 4034;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches	2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	64	AGGCCTTCGGATGGCAGCCTGGCTGGCTCTGGTCTCGCAGTGCCATCTCCCTGGTCTC 123
Db	1943	AGGCCTTCGGATGGCAGCCTGGCTGGCTCTGGTCTCGCAGTGCCATCTCCCTGGTCTC 2002
Qy	124	TCTGGTCATGGACGGCTGGTGCAGGATTCGCACTCGAGCAGTCTATTGCCAGTGT 183
Db	2003	TCTGGTCATGGACGGCTGGTGCAGGATTCGCACTCGAGCAGTCTATTGCCAGTGT 2062
Qy	184	GGCAGCTTCCCTGGCTGCCACATGCCCTGCAGTGTGGCG 243
Db	2063	GGCAGCTTCCCTGTGGCTGCCACATGCCCTGCAGTGTGGCG 2122
Qy	244	AGCTTCAAGCCCTCACCGGTTACCTTCAGCCCTGCAGATCCTGCCA 303
Db	2123	AGCTTCAAGCCCTCACCGGTTACCTTCAGCCCTGCAGTGTGGCG 2182
Qy	304	GGCCTCCCTCACACCGGAGAGCAGGTTCCTGCCAATACCGAGGGACACTGG 363
Db	3183	GGCCTCCCTCACACCGGAGAGCAGGTTCCTGCCAATACCGAGGGACACTGG 3142
Qy	364	AGGTCTAGCAGGACAGCTGATGCCAGCTCCAGGCCCTAACCTGG 423
Db	2243	AGGTCTAGCAGGACAGCTGATGCCAGCTCCAGGCCCTAACCTGG 2242
Qy	2303	TCCCTCCCTAACGGACACGGCTGATGCCAGCTCCAGGCCCTAACCTGG 2302
Qy	424	TCCCTCCCTAACGGACACGGCTGATGCCAGCTCCAGGCCCTAACCTGG 483
Db	2363	TCCCTCCCTAACGGACACGGCTGATGCCAGCTCCAGGCCCTAACCTGG 2362
Qy	484	GCTCT3CGGGCCTCTGGTCTGGAGGGCAGTGGCTGCTGAG 483
Db	2423	GCTCT3CGGGCCTCTGGTCTGGAGGGCAGTGGCTGCTGAG 2423
Qy	544	GGCCAGGGTCCGGGCGATCTGCTGATGCTCCGGTGGGGTGAACCGA 543
Db	2363	GGCCAGGGTCCGGGCGATCTGCTGATGCTCCGGTGGGGTGAACCGA 2363
Qy	604	CCTGCTGGTCCGGGCGATCTGCTGATGCTCCGGTGGGGTGAACCGA 603
Db	2483	CCTGCTGGTCCGGGCGATCTGCTGATGCTCCGGTGGGGTGAACCGA 2483
Qy	664	TGTCACTGCCTATATGGTCTGCCCATGGCTTATGGCTTACGGCTAGCCAGTC 663
Db	2543	TGTCACTGCCTATATGGTCTGCCCATGGCTTACGGCTAGCCAGTC 2543
Qy	724	ACAGGTAGTATTGACAAGAGGCACTGGCTCTGGCTTACGGCTAGCCAGTC 723
Db	2603	ACAGGTAGTATTGACAAGAGGCACTGGCTCTGGCTTACGGCTAGCCAGTC 2603
Qy	784	ATTGGGGTGGAGGGCTGCCCCTGGCTTACGGCTTACGGCTAGCCAGTC 783
Db	2663	ATTGGGGTGGAGGGCTGCCCCTGGCTTACGGCTTACGGCTAGCCAGTC 2663
Qy	844	GCTGCCGGCTGGCCAGTTCCTGTCCTGCCAAGTAATGGCTCTGCCAC 903
Db	2723	GCTGCCGGCTGGCCAGTTCCTGTCCTGCCAAGTAATGGCTCTGCCAC 2782
Qy	904	CCTGTCCTGAGGTGGCTGAGCTGCACAGCTGGGGCTGGGGCTCTCTCTC 963
Db	2783	CCTGTCCTGAGGTGGCTGAGCTGCACAGCTGGGGCTGGGGCTCTCTC 2842
Qy	964	CCCAGTCTTAGGGCTGCTGACTGGAGGCCTCAGGGGTTTCAGTCTGGACTTATA 1023
Db	2843	CCCAGTCTTAGGGCTGCTGACTGGAGGCCTCAGGGGTTTCAGTCTGGACTTATA 2902
Qy	1024	CAGGAGGCCAGAAGGGCTCATGCACTGGAATGGGGACTCTGCAGGTGGATTACCA 2962
Db	2903	CAGGAGGCCAGAAGGGCTCATGCACTGGAATGGGGACTCTGCAGGTGGATTACCA 2962
Qy	1084	GGCTCAGGGTTACAGCTAGCCTCTAGTGAGAACACACTAGAGAAGGGTTTGGAG 1143
Db	2963	GGCTCAGGGTTACAGCTAGCCTCTAGTGAGAACACACTAGAGAAGGGTTTGGAG 3022
Qy	1144	CTGATAAACTCAGTCACCTGTTCCCACATCTCTAAGCCCCCTAACCTGCAGCTCGTT 1203
Db	3023	CTGATAAACTCAGTCACCTGTTCCCACATCTCTAACCCCCTTAACCTGCAGCTCGTT 3082
Qy	1204	AATGTTAGCTCTGCTGGAGTTCTAGGATGAAACACTCCCTCATGGATTGACATA 1263
Db	3083	AATGTTAGCTCTGCTGGAGTTCTAGGATGAAACACTCCCTCATGGATTGACATA 3142
Qy	1264	TGAAGTTATTGTTAGGGAAAGAGTCTCTGAGGGCCACACACAAAGAACGGTCCCA 1323
Db	3143	TGAAGTTATTGTTAGGGAAAGAGTCTCTGAGGGCAACACACAAAGAACGGTCCCA 3202
Qy	1324	GCCCCACAGCACTGTTTTGCTGATCCACCCCCCTTACCTTATCAGGATGTGGCC 1383
Db	3203	GCCCCACAGCACTGTTTTGCTGATCCACCCCCCTTACCTTATCAGGATGTGGCC 3261
Qy	1384	TGTTGGTCTCTGTTGCTGATCCACAGAGACACAGGCTTAATTTAATTACTTATT 1443
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Qy	1444	TACAAAGTGAAGGGATCCATGCTAGCTTCTGTTGTTGTTCTAATTTAATTGTA 1503
Db	3322	TACAAAGTGAAGGGATCCATGCTAGCTTCTGTTGTTCTAATTTAATTGTA 3381
Qy	1504	GGGTGGGGATCCCCAACAACTAGGCTCCCTGAGATAGCTGTGGTCTAATTTGTA 1563
Db	3382	GGGTGGGGATCCCCAACAACTAGGCTCCCTGAGATAGCTGTGGTCTAATTTGTA 3441
Qy	1564	CCAGAATCTCTCTGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1623
Db	3442	CCAGAATCTCTCTGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 3501
Qy	1624	TCTACTCTCCCAATGATAATTCCAATGGCTTACCCAGGTAGGGTGTGAAGGA 1683
Db	3502	TCTACTCTCCCAATGATAATTCCAATGGCTTACCCAGGTAGGGTGTGAAGGA 3561
Qy	1684	AGGTAGAGGGGGCTCCACTCCCTACTCTCTAGGACTGGCTGTACCCAGTC 1743
Db	3562	AGGTAGAGGGGGCTCCACTCCCTACTCTCTAGGACTGGCTGTACCCAGTC 3621
Qy	1744	CAGCTGGTCCCCACTCCCTACTCTCTAGGACTGGCTGTACCCAGTC 1803
Db	3622	CAGCTGGTCCCCACTCCCTACTCTCTAGGACTGGCTGTACCCAGTC 3681
Qy	1804	CACTGCCAAATTCCCTACCCCAACTTCCCTACTCTCTAGGACTGGCTGTACCCAGTC 1863
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Qy	1864	CCACAACCTGTTGGAGGACTGGCAGGACAGGACAAACTGGCTTCCCAAGGCT 1923
Db	3742	CCACAACCTGTTGGAGGACTGGCAGGACAGGACAAACTGGCTTCCCAAGGCT 3801

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Db 3802 TTGTCATCTCAGCCCCAGACTATCTGTCCTGGAAATCTCACAGAACAG 3861

Qy 1984 AGCACCCCTGCCTGAGCTAAGGGAGTCTATCTCTCAGGGGGTTAAGTGGCGTT 2043

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Db 3982 AGGATAATGTTATGGTGACAAATTAAAGCTTCTATATGTTA 4030

REFERENCE 1 (bases 1 to 4034)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stoik,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.

VERSION AR40443.1 GI:40143820

KEYWORDS Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6620922-A 704 16-SEP-2003;

FEATURES Source 1..4034 /organism="unknown" /mol_type="genomic DNA"

ORIGIN

Query Match 91.4%; Score 1968; DB 6; Length 4034;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 64 AGGGTTCGGATGGCAGGCTGGCTGTTCTGCAGTGGCCATCTCCCTGGTCTCTC 123

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Qy 184 GGCAGCTTCCCTGGCCACATGGCCACAGTGGCTGGGGCTCAAGGGGTTCAAGGGGACTCTGGACTATA 1023

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Qy 1024 CAGGGGCCAGAAGGGCTCCAGTGGATGGGACTCTGGAGGTTCAAGGGGTTCAAGGGGACTCTGGACTATA 1083

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QY	1744	CACTGGCTCCCCACTCCACTCCCTACTCTCTAGGACTGGGCTGTGAGG	1803	Db	2123	AGCTTCAGCCGCCCACCGGGTTCACCTCTCAGGTCACCGGCTCTTGCC	3681
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QY	1924	TTGTCCATCTCAGCCCCAGAGTATCTGTGCTGGGAATCTCACAGAACTCAGG	1983	Db	2303	TCCCTCCCTAATGGAACAGTGCAGGACAGCTTCCCAACTCCACCTCCACCG	2362
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ORGANISM	Unclassified.	Unclassified.	Unclassified.	Unclassified.	Unclassified.	Unclassified.	Unclassified.
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AUTHORS	TITLE	JOURNAL	JOURNAL	JOURNAL	JOURNAL	JOURNAL	JOURNAL
VERSION	1	1	1	1	1	1	1
KEYWORDS	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER	COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER
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Query	1943	AGGGTTCGGATGGGAGCCTGGGACTGTCTGCAGTGCCTACCTCCCTGGCTTC	2002	Db	2963	GGCTCAGGGTTACAGCTACCTGGCTTCAGGACACACCTAGAGAAGGGTTTGGAG	3022
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AUTHORS		Xu,J., Dillon,B.C., Mitchell,J.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Helper,W.T. and Henderson,R.A.	
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VERSION AR564090.1			
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ORGANISM Unclassified.			
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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13	475	22.1	875 5 BQ942028	
14	474	22.0	1060 5 BM914562	
15	470	21.8	515 5 BX098291	
16	437	20.3	734 6 CD634718	
17	430	20.0	437 7 CF135166	
18	390	18.1	418 2 BF922235	
19	390	18.1	599 6 CB050165	
20	386	17.9	740 6 CD634716	
21	382	17.8	1667 5 BM912193	
22	377	17.5	494 7 CF134970	
23	373	17.3	850 4 BF972601	
24	353	16.4	370 2 AW135465	

Query Match		Db	1201
Best Local Similarity	97.0%;	Score	2088;
Matches	2088;	DB	3;
Conservative	100.0%;	Length	2477;
Mismatches	0;	Pred. No.	0;
		Indels	0;
		Gaps	0;
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Db	361	GGCGTTCGGATGGGCAGCTGGCTGTCTGCAGTGCCATCTCCCTGGCTCTCT	420
QY	125	CTGGTCATGGACCGGCTGGTCAAGGATTGGCACTCGGACTCTGAGCACTCT	184
Db	421	CTGGTCATGGACCGGCTGGTCAAGGATTGGCACTCGGACTCTGAGCACTCT	480
QY	185	GCAGCTTCCTGTGGCTGGCGTGCACAGGATTCGGCACTCGGACTCTGAGCA	244
Db	481	GCAGCTTCCTGTGGCTGGCGTGCACAGGATTCGGCACTCGGACTCTGAGCA	540
QY	245	GCTTCAGGCCCTCACCGGTTCACCTCTAGCCTGAGAACACTCTCCATGGAT	304
Db	541	GCTTCAGGCCCTCACCGGTTCACCTCTAGCCTGAGAACACTCTCCATGGAT	600
QY	305	GCTTCCTCACCGGAGAACACTGGCTCTGCCAATACCGAGGGACACTGGA	364
Db	601	GCTTCCTCACCGGAGAACACTGGCTCTGCCAATACCGAGGGACACTGGA	650
QY	365	GGTAGCTACCGAGGACAGCTGATGACCAGGTTCTGAGGGAAACACACAGA	424
Db	661	GGTAGCTACCGAGGACAGCTGATGACCAGGTTCTGAGGGAAACACACAGA	720
QY	425	CCCTCCCTAATGGACACGTTGAGGAGAACCTCCACCCGG	484
Db	721	CCCTCCCTAATGGACACGTTGAGGAGAACCTCCACCCGG	780
QY	485	CTCTGGGGCTCTGCTGTGATCTCCGTACGTGTGGGGTGGCTGCTGAGG	544
Db	781	CTCTGGGGCTCTGCTGTGATCTCCGTACGTGTGGGGTGGCTGCTGAGG	840
QY	545	GCGAGGGTCTGGGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCCTC	604
Db	841	GCGAGGGTCTGGGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCCTC	900
QY	605	CTGCTGTCCTGGCCCATCTGGTATGGCTCATGGTCTGGGGGGGGGG	664
Db	901	CTGCTGTCCTGGCCCATCTGGTCTGGGGGGGGGGGGGGGGGGGGGG	960
QY	665	GTCACTGCTATATGGTGTCTGGCCAGGCCCTGGTCTGGGGGGGGGG	724
Db	961	GTCACTGCTATATGGTGTCTGGCCAGGCCCTGGTCTGGGGGGGGGG	1020
QY	725	CAGGTAGTATGGACAAGAGGCACTGGCCAAATACTCAGCGTAGAAACT	784
Db	1021	CAGGTAGTATGGACAAGAGGCACTGGCCAAATACTCAGCGTAGAAACT	1140
QY	785	TGGGGTGGAGGGCTGCTCACTGGTCCAGCTCCATTTACTTGTCTA	844
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QY	845	CTGCGGGCTGGCCAGTTCTGTTGCTGCAAGTAAAGTGGCTCTGCCACC	904
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QY	905	CTGTGCTGAGGTGCTGACAGCTGGGGGCTTACTCTCAGGGGGTTAAGT	2340
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QY	1205	ATGTAAGCTCTGCACTGGAGTTCTAGGATGAAACACTCTCCATGGAT	1264
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QY	1265	GAAAGTTATTGGAGAGAGTCTGAGGGCAACACACAGAACAGGTTCCAG	1324
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Db	1621	CCCACAGCACTGTCTTCTGATCCACCCCCCTTACCTTATCGAGATGTGGCCT	1680
QY	1385	GTGCGCTCTCTGTTGCTGATCCACCCCCCTTACCTTATCGAGATGTGGCCT	1444
Db	1681	GTGCGCTCTCTGTTGCTGATCCACCCCCCTTACCTTATCGAGATGTGGCCT	1740
QY	1445	AACAACTAGAAGGAATCCATTGCTAGTCTGAGGGAAACACACAGAACAGG	1504
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QY	1505	GTTGGCTCTCTGTTGCTGACATCACAGGACACAGGATTAATTAACTTATT	1444
Db	1801	GTTGGCTCTCTGTTGCTGACATCACAGGACACAGGATTAATTAACTTATT	1920
QY	1565	CAGAATCTCTCTGGGCTCTGGGGTGGCTGAGGATAGCTGGCTATGGGAAT	1624
Db	1861	CAGAATCTCTCTGGGCTCTGGGGTGGCTGAGGATAGCTGGCTATGGGAAT	1860
QY	1625	TCTACTCATCCAAATGATAATTCCAAATGCTGTACGGTACCCATCTGG	1684
Db	1921	TCTACTCATCCAAATGATAATTCCAAATGCTGTACGGTACCCATCTGG	1980
QY	1685	GGTAGAGGGGGCTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTGG	1744
Db	1981	GGTAGAGGGGGCTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTGG	2040
QY	1745	AGCCTGGTCCCCCACTCCACTCCCCCTACTCTCTAGGACTGGGGTGTGAA	1804
Db	2041	AGCCTGGTCCCCCACTCCACTCCCCCTACTCTCTAGGACTGGGGTGTGAA	2100
QY	1805	ACTGCCAAATTCTCCCTAACCCCCAACCTTCCCTACTCTCTAGGACTGG	1864
Db	2101	ACTGCCAAATTCTCCCTAACCCCCAACCTTCCCTACTCTCTAGGACTGG	2160
QY	1865	CACACCCCTGGGACTCTGAGGACAGGACAGAACAGGAAACTCAGGA	1924
Db	2161	CACACCCCTGGGACTCTGAGGACAGGACAGAACAGGAAACTCAGGA	2220
QY	1925	TGTCCATCTAGGCCAGAGTATCTGTTGCTGGCTTCAACAGAACAGGAA	1984
Db	2221	TGTCCATCTAGGCCAGAGTATCTGTTGCTGGCTTCAACAGAACAGGAA	2280
QY	1985	GCACCCCTGCTGAGCTAAGGGGGCTTACTCTCAGGGGGTTAAGTGC	2044
Db	2281	GCACCCCTGCTGAGCTAAGGGGGCTTACTCTCAGGGGGTTAAGTGC	2340

Qy	2045	CAATAATGTCGCTTATTAGGGGAATATTAGGGAGTTAATGAGCAATCA	2104	Db	.301	GGGACTCTGCAGGTACCGAGCTCAGGTTAACAGCTAGGCTCTAGTGAGAC	360
Db	2341	CAATAATGTCGCTTATTAGGGAGTTAATGAGCAATCA	2400	Qy	1119	ACACCTAGAGAAGGTTTGGAGCTGAATAACTCAGTCACCTGGTTCCATCTCA	1178
Qy	2105	GAGTATAATGTTATGGTACAATAAGGCTTCTATGTTA	2152	Db	361	ACACCTAGAGAAGGTTTGGAGCTGAATAACTCAGTCACCTGGTTCCATCTCA	420
Db	2401	GAGTATAATGTTATGGTACAATAAGGCTTCTATGTTA	2448	Qy	1179	AGCCCTTAACCTGCAGCTCGTTATGAGCTCTGCAATGGAGTTCTAGGATGAA	1238
RESULT 2	CN373215	CN373215	722 bp	mRNA	linear	EST 16-MAY-2004	
LOCUS	CN373215	CN373215					
DEFINITION	17000532237472	GRN_ES	Homo sapiens	cdNA 5'	mRNA	sequence.	
ACCESSION	CN373215	CN373215					
VERSION	CN373215.1	GI:47373149					
KEYWORDS	EST.						
SOURCE	Homo sapiens	(human)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1	(bases 1 to 722)					
AUTHORS	Branderberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guebler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.						
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation						
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)						
COMMENT	Contact: Branderberger R						
Regenerative Medicine							
Geron Corporation							
230 Constitution Drive, Menlo Park, CA 94025, USA							
Tel: 650 473 8658							
Fax: 650 473 7760							
Email: rbranderberger@geron.com							
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/clone_lib="GRN_ES"							
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ORIGIN							
Query Match	33.6%	Score 722; DB 7; Length 722;					
Best Local Similarity	100.0%	Pred. No. 0;					
Matches	722;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	759	ACTCAGCGTAGAAACTCCAGCACATGGGTGGAGGGCTGGCTCACTGGTCCAGC	818	Db	1	ACTCAGCGTAGAAACTCCAGCACATGGGTGGAGGGCTGGCTCACTGGTCCAGC	60
Db	819	TCCCCGCTCTGTAGCCCCATGGGGCTGCCCCAGTTCTGTGCTGCCA	878	Qy	61	TCCCCGCTCTGTAGCCCCATGGGGCTGCCCCAGTTCTGTGCTGCCA	120
Db	879	AACTAATGTCGCTCTGCTGCCACCCCTGGCTGAGGTGCGTAGCTGCACAGCTGG	938	Db	121	AACTAATGTCGCTCTGCTGCCACCCCTGGCTGAGGTGCGTAGCTGCACAGCTGG	180
Db	939	GGCTGGGGCTCCCTCTCTCCCCAGCTCTAGGGCTGACTGGAGGCC	998	Qy	181	GGCTGGGGCTCCCTCTCTCCCCAGCTCTAGGGCTGACTGGAGGCC	240
Db	999	AAGGGGGTTCACTCTGACTTACAGGGGCCAGAAGGGCTCATGCACTGGATGC	1058	Qy	241	AAGGGGGTTCACTCTGACTTACAGGGGCCAGAAGGGCTCATGCACTGGATGC	300
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Query Match	Score	DB	Length
Best Local Similarity	32.7%	704	1626
Matches	100.0%	Pred. No.	0
704; Conservative	0	Mismatches	0
	Indels	0	Gaps
		0	0
Y	66	CGCGTCGGATGGCAGCCTGGGCTGTTCCCTGCAGTGCACATCTCCTGGCTTCTCTC	125
b	923	CGGTTCCGATGGCAGCCTGGGCTGCGCATCTCCCTGGCTTCTC	982
Y	126	TGGTCATGGACCGGCTGGTCAGCGATTGGCACTCGAGCAGTCTATTGCCAGTGTG	185
b	983	TGGTCATGGACCGGCTGGTCAGCGATTGCCACTCGAGCAGTCTATTGCCAGTGTG	1042
Y	186	CAGCTTCCCTGTGCCACATGCCCTGCCACAGTGTGCCGTGGTACAG	245
b	1043	CAGCTTCCCTGTGCCACATGCCCTGCCACAGTGTGCCGTGGTACAG	1102
Y	246	CTTCAGCCGCCCTCACGGGTCACTTCAGCCCTGCAGTCCTGCCCTACACACTGG	305
b	1103	CTTCAGCCGCCCTCACGGGTCACTTCAGCCCTGCAGTCCTGCCCTACACACTGG	1162
Y	306	CCTCCCTTACCAACGGGAGAACCGCAGCTGTTCCGCCAAATACCGAGGGCACACTGGAG	365
b	1163	CCTCCCTTACCAACGGGAGAACCGCAGGTGTTCCTGCCCAAATACCGAGGGCACACTGGAG	1222
Y	366	GTGCTAGCACTGAGGACAGCCTGATGACCAGCTTCCAGGCCCTAACGCTGGAGCTC	425

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2005 row: f column: 03
 High quality sequence start: 35
 High quality sequence stop: 657.
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 /clone="IMAGE:5481218"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_41"
 /note="Organ: skin; vector: POTB7; site₁: Xhol; site₂:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGGAG (G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 SuperScript II RT (Life Technologies). Note: this is a
 NIH MGC library"

Qy 2109 ATAATGTTATGGTGACAAATTAAAGGTTCTATATGTTA 2152
 Db 61 ATAAATGTTATGGTGACAAATTAAAGGTTCTATATGTTA 18

ORIGIN

Query Match 29.9%; Score 644; DB 5; Length 670;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1509 GGGGATCCCCAACATCAGGCCCCCTGAGATAGCTGGTCAATTGGCTGATCATGCCAGA 1568
 Db 661 GGGGATCCCCAACATCAGGCCCCCTGAGATAGCTGGTCAATTGGCTGATCATGCCAGA 602

Qy 1569 ATCTCTTCTCTGGGGCTGGCCCCCAAATGCCTAACCCAGGACCTGGAAATTCTA 1628
 Db 601 ATCTCTTCTCTGGGGCTGGCCCCCAAATGCCTAACCCAGGACCTGGAAATTCTA 542

Qy 1629 CTACATCCAAATGATAATTCCAAATGCTGTACCCAAGGGTAGGGTGTGAAGGGAGGT 1688
 Db 541 CTACATCCAAATGATAATTCCAAATGCTGTACCCAAGGGTAGGGTGTGAAGGGAGGT 482

Qy 1689 GGGGGGGCTTCAGGCTCAACGGCTCCCTAACCAACCCCTCTTGCCAGCC 1748
 Db 481 GGGGGGGCTTCAGGCTCAACGGCTCCCTAACCAACCCCTCTTGCCAGCC 422

Qy 1749 TGTTCCTCCACTCCCTACTCTCTAGGACTGGGCTGTGAAGGACTG 1808
 Db 421 TGTTCCTCCACTCCCTACTCTCTAGGACTGGGCTGTGAAGGACTG 362

Qy 1809 CCCAAATTCCCTACCCCAACTTCCCTACCCCAACTTCCCTACCCCA 1868
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ORIGIN

Query Match 29.6%; Score 638; DB 6; Length 651;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1869 ACCCTGTTGGAGCTACTGCAGGACCAAGGACCAAGTGGTTCCCAAGCCTTGTC 1928
 Db 301 ACCCTGTTGGAGCTACTGCAGGACCAAGTGGTTCCCAAGCCTTGTC 242

Qy 1929 CATCTCAGCCCCAGAGTATCTGCTGGAACTCCACACAGAACTCAGAGCAC 1988
 Db 241 CATCTCAGCCCCAGAGTATCTGCTGGAACTCCACACAGAACTCAGAGCAC 182

Qy 1989 CCCCTGCCTAGCTAAGGGAGGTCTATCTCTAGGGGGTTAAGTGCCTTGAAT 2048
 Db 181 CCCCTGCCTAGCTAAGGGAGGTCTATCTCTAGGGGGTTAAGTGCCTTGAAT 122

Qy 2049 ATGTCGCTCTATTATTTAGGGGGTGAATTATTAATCTGTAAGTGAATCAGGT 2108
 Db 121 ATGTCGCTCTATTATTTAGGGGGTGAATTATTAATCTGTAAGTGAATCAGGT 62

Qy 2109 ATAATGTTATGGTGACAAATTAAAGGTTCTATATGTTA 2152
 Db 61 ATAAATGTTATGGTGACAAATTAAAGGTTCTATATGTTA 18

RESULT 7

CB048223 LOCUS CB048223 mRNA 651 bp linear EST 17-JAN-2003
 DEFINITION NISC_gj03e11.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270644
 5' mRNA sequence.

ACCESSION CB048223
 VERSION CB048223.1 GI:27786510
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; 1 (bases 1 to 651)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

TITLE Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgapsr@mail.nih.gov

COMMENT CDNA Library Preparation:
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)

Seq primer: M13RPI reverse primer (ABI).

FEATURES Location/Qualifiers

source 1..651

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 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polyLinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 29.9%; Score 644; DB 5; Length 670;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1462 TCCATGCTAGCTTCTGTTGGTCTAATATTGGTAGGGTGGGGATCCCCAAC 1521
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Qy 1522 AATCAGGTCCCTGAGATAGCTGGTCAATTGGCTGATGCCAGAATCTCTCT 1581
 Db 74 AATCAGGTCCCTGAGATAGCTGGTCAATTGGCTGATGCCAGAATCTCTCT 133

Qy 1582 GGGTCTGGCCCCAAATGCCTAACCCAGGACCTGGAAATTCTACTCTCAAT 1641
 Db 134 GGGTCTGGCCCCAAATGCCTAACCCAGGACCTGGAAATTCTACTCTCAAT 193

Qy 1642 ATAATCCAATGCTGTTACCAAGGTAGGGTGTGAAGGAAGGTAGGGTGGGGCT 1701
 Db 194 ATAATCCAATGCTGTTACCAAGGTAGGGTGTGAAGGAAGGTAGGGTGGGGCT 253

QY 1702 CAGGTCTCAACGGCTTCCCTAACCAACCCCTCTCTCTTGGCCAGGCCGGTCC 1761
 Db 254 CAGGTCTCAACGGCTTCCCTAACCAACCCCTCTCTTGGCCAGGCCGGTCC 313

QY 1762 T^TCCACTCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCAAATTCCC 1821
 Db 314 TTCCACTCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCAAATTCCC 373

QY 1822 CTACCCCCAACTTTCCCTACCCCCAACTTCCCCAACAGCTCCACAAACCTGTGGAG 1881
 Db 374 CTACCCCCAACTTTCCCTACCCCCAACTTCCCCAACAGCTCCACAAACCTGTGGAG 433

QY 1882 CTACTGCAGGACAGAACGACAAGTGGGTTTCCCAAGCCACAGCTCCACAAACCTGTGGAG 1941
 Db 434 CTACTGCAGGACAGAACGACAAGTGGGTTTCCCAAGCCACAGCTCCACAAACCTGTGGAG 493

QY 1942 AGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGGACACCCCTGCTGAGC 2001
 Db 494 AGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGGACACCCCTGCTGAGC 553

QY 2002 TAGGGAGGTCTATCTCTAGGGGTTAAGTGCCTTGCAATAATGTCGTCTTAT 2061
 Db 554 TAGGGAGGTCTATCTCTAGGGGTTAAGTGCCTTGCAATAATGTCGTCTTAT 613

QY 2062 TTATTTAGGGGGTGAATTTTATTTACTGTAGTGAGC 2099
 Db 614 TTATTTAGGGGGTGAATTTTATTTACTGTAGTGAGC 651

RESULT 8
 BQ950912 BQ950912 916 bp mRNA linear EST 21-AUG-2002

LOCUS BQ950912 DEFINITION AGENCOURT 8754471 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6205362 5', mRNA sequence.

ACCESSION BQ950912
 VERSION BQ950912.1 GI:22366390
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetacei; Hominidae; Homo.
 1 (bases 1 to 916)
 NIH-MGC http://mgc.ncbi.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13628 row: b column: 19
 High quality sequence stop: 579.

FEATURES source
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 /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: Sall; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTAGCGCAGCGGGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN Query Match 28.7%; Score 617; DB 5; Length 916; Best Local Similarity 100.0%; Pred. No. 0; Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1101 TAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGGAGCTGAATAACTCAGTCA 1160
 Db 1 TAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGGAGCTGAATAACTCAGTCA 60

QY 1161 CCTGTTTCCCACACTCTAACCTGCAGCTCGTTAATGTCGTCTTGTGATCTTGATG 1220
 Db 61 CCTGTTTCCCACACTCTAACCTGCAGCTCGTTAATGTCGTCTTGTGATCTTGATG 120

QY 1221 GGAGTTCTAGGATGAAACACTCCTCCATGGATTTGACATATGAAAGTTATTGTAGG 1280
 Db 121 GGAGTTCTAGGATGAAACACTCCTCCATGGATTTGACATATGAAAGTTATTGTAGG 180

QY 1281 GGAGTTCTAGGATGAAACACTCCTCCATGGATTTGACATATGAAAGTTATTGTAGG 1340
 Db 181 GGAAAGTCTGAGGGAAACACACACAGAAACACAGGTTGGCCTGTGGCCCTCTGTGCTT 240

QY 1341 TTGCTGATCCACCCCTTACCTTATCAGGATGTGGCTGTGGCCCTCTGTGCTT 1400
 Db 241 TTGCTGATCCACCCCTTACCTTATCAGGATGTGGCTGTGGCCCTCTGTGCTT 300

QY 1401 CCATCACAGAGACACAGGATTAAATTAACTTATTAACTTAAACAAGTAGAAGGGA 1460
 Db 301 CCATCACAGAGACACAGGATTAAATTAACTTATTAAACAAGTAGAAGGGA 360

QY 1461 ATCCATGCTAGCTTTCTGTGTTGGTCTAATATTGGGTAGGGGGATCCCCAA 1520
 Db 361 ATCCATGCTAGCTTTCTGTGTTGGTCTAATATTGGGTAGGGGGATCCCCAA 420

QY 1521 CAATCAGGTCCCCCTGAGATAGCTGGTCATGGGCTGATCATGCCAGAACTCTCTCC 1580
 Db 421 CAATCAGGTCCCCCTGAGATAGCTGGTCATGGGCTGATCATGCCAGAACTCTCTCC 480

QY 1581 TGGGCTCTGGCCCCAAATGCCTAACCCAGGACTTGGAAATTCTACTCATCCAAAT 1640
 Db 481 TGGGCTCTGGCCCCAAATGCCTAACCCAGGACTTGGAAATTCTACTCATCCAAAT 540

QY 1641 GATAATTCCAATGCTTACCAAGGTTAGGGTGTGAAGGAAGGTTAGGGGGCT 1700
 Db 541 GATAATTCCAATGCTTACCAAGGTTAGGGTGTGAAGGAAGGTTAGGGGGCT 600

QY 1701 TCAGGTCTCAACGGCTT 1717
 Db 601 TCAGGTCTCAACGGCTT 617

RESULT 9
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LOCUS BQ950805 DEFINITION AGENCOURT 8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6204253 5', mRNA sequence.

ACCESSION BQ950805
 VERSION BQ950805.1 GI:22366283
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetacei; Hominidae; Homo.
 1 (bases 1 to 959)
 NIH-MGC http://mgc.ncbi.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM13625 row: d column: 14
 High quality sequence start: 2
 High quality sequence stop: 490.
 Location/Qualifiers
 FEATURES source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult", 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski_sciatic_nerve"
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGGTCCG-3' and 5'-GACTAGTCTAGATGGAGCCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Query Match 26.2%; Score 564; DB 5; Length 959;

Best Local Similarity 100.0%; Pred. No. 1.5e-291; Mismatches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 CGTGGGGCTGGAGGCAGTGGCCTGCTCCACCTCCACCCGGCTCTGGGGGCTCTGC 501
 DB 7 CGTGGGTCTGGAGGCAGTGGCCTGCTCCACCTCCACCCGGCTCTGC 66
 QY 502 CTGTGATGTCTCCGTACCGTGTGGTGGGGTGGCTGG 561
 DB 67 CTGTGATGTCTCCGTACCGTGTGGTGGGGTGGCTGG 126
 QY 562 CGGGGCATCTGGCATCTGGACCTGCCATCTGGATAGTGCCTCTGGTCCAGGGGGC 621
 DB 127 CGGGGCATCTGGCATCTGGACCTGCCATCTGGATAGTGCCTCTGGTCCAGGGGGC 186
 QY 622 CCCATCCCTGTTATGGCTCCATGTCAGCTCAGCCAGTGTCACTGCCATATGGT 681
 DB 187 CCCATCCCTGTTATGGCTCCATGTCAGCTCAGCCAGTGTCACTGCCATATGGT 246
 QY 682 GCTGCGCCAGCCTGGTCTGGTCTGGCATTTACTTGCTACACAGGTGATTGACAA 741
 DB 247 GCTGCGCCAGGCTGGTCTGGTCTGGCATTTACTTGCTACACAGGTGATTGACAA 306
 QY 742 GAGCAGCTTGGCCAAATACTCAGCGTAACTCCAGCACATGGGTGGAGGCGCTG 801
 DB 307 GAGCAGCTTGGCCAAATACTCAGCGTAACTCCAGCACATGGGTGGAGGCGCTG 366
 QY 802 CCTCACTGGGCTCCAGCTCCCGCTCTGGTAGCCCCATGGGCTGCCAGCTGCC 861
 DB 367 CCTCACTGGGCTCCAGCTCCCGCTCTGGTAGCCCCATGGGCTGCCAGCTGCC 426
 QY 862 AGTCTCTGTTGCTGCCAAAGTAATGGCTCTGCTGAGGCTCTGGCTGCTGAGGTC 921
 DB 427 AGTCTCTGTTGCTGCCAAAGTAATGGCTCTGCTGAGGCTCTGGCTGCTGAGGTC 486
 QY 922 GTAGCTGACAGCTGGGCTGGGGCTCTCTCTCCAGTGTCTAGGGCTGTC 981
 DB 487 GTAGCTGACAGCTGGGCTGGGGCTCTCTCTCCAGTGTCTAGGGCTGTC 546

Query Match 25.1%; Score 541; DB 2; Length 718;

Best Local Similarity 100.0%; Pred. No. 3.6e-279; Mismatches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 TCTGGTCATGGACCGGGCTGGTGCAGGATCGGCACCTCGAGGAGTCTATTGGCCAGTGT 183
 DB 1 TCTGGTCATGGACCGGGCTGGTGCAGGATCGGCACCTCGAGGAGTCTATTGGCCAGTGT 60
 QY 184 GGCAGCTTCCCTGGCTGCCAGATGCCCTGGCAGGCTTCTGGCTGCCAGTGTCTGGTGC 243
 DB 61 GGCAGCTTCCCTGGCTGCCAGATGCCCTGGCTGCCAGTGTCTGGTGC 120
 QY 244 AGCTTCAAGCGCCCTCACCGGGTCACTTCTCAGGCCCTGCAGATCTGGCTCACACT 303
 DB 121 AGCTTCAAGCGCCCTCACCGGGTCACTTCTCAGGCCCTGCAGATCTGGCTCACACT 180
 QY 304 GGCTTCCCTTACACCCGGAGAAGCAGGCTGTTCTGCCAAATACCGAGGGACACTGG 363
 DB 181 GGCTTCCCTTACACCCGGAGAAGCAGGCTGTTCTGCCAAATACCGAGGGACACTGG 240
 QY 364 AGGTGCTAGCAGTGGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCTGGAGC 423
 DB 241 AGGTGCTAGCAGTGGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCTGGAGC 300
 QY 424 TCCCTCCCTAATGGACACCGTGGGTGCTGGAGGAGCTGGCTCTCCACCTCCACCCCGC 483

Db	301	TCCCTTCCTTATGGACAGCTGCTGGAGGCTGGCTGCTCCACCTCCACCGC	360	Db	159	GGAAGAGTCCTAGGGCACACACAAGAACAGGTCCTCAGCCCACAGCACTGTCTT	218
Qy	484	GCTCTGGGGGACCTCTGCCCTGTGATGTCCTGGTACGGTGGTGGGACCCAGGA	543	Qy	1341	TTTGTGATCCACCCCCCTTACCTTATCAGGATGTTGGCTGTTGGCTCTCTGTG	1400
Db	361	GCTCTGGGGGACCTCTGCCCTGTGATGTCCTGGTACGGTGGTGGGAGCCACCGA	420	Db	219	TTTGTGATCCACCCCCCTTACCTTATCAGGATGTTGGCTGTTGGCTCTCTGTG	278
Qy	544	GCCAGGGTGTCCGGGGGGCATCTGCTGGACCTGCCATCCTGGATAGTGCCT	603	Qy	1401	CCATCACAGAGACAGGCAATTAACTTAACTTAACTTAACTTAACTTAAAGTGAAGGGA	1460
Db	421	GCCAGGGTGTCCGGGGGGCATCTGCTGGACCTGCCATCCTGGATAGTGCCT	480	Db	279	CCATCACAGAGACAGGCAATTAACTTAACTTAACTTAACTTAAAGTGAAGGGA	338
Qy	604	CCTGCTGCCAGGTGGTCCGGGGGGCATCTGCTGGACCTGCCATCCTGGATAGTGCCT	663	Qy	1461	ATCCATGCTAGCTTCTGTGTTGGTCTAATATTGGTAGGGGGATCCCAA	1520
Db	481	CCTGCTGCCAGGTGGGGGGCATCTGCTGGACCTGCCATCCTGGATAGTGCCT	540	Db	339	ATCCATGCTAGCTTCTGTGTTGGTCTAATATTGGTAGGGGGATCCCAA	398
Qy	664	T 664		Qy	1521	CAATCAGAGACAGGCAATTAACTTAACTTAACTTAACTTAAAGTGAAGGGA	1580
Db	541	T 541		Db	399	CAATCAGGTCCTGAGATAGCTGCTCATGGGTGATCATGCCAGAATCTCTTCTCC	458
RESULT 11							
LOCUS	CN373214	581 bp mRNA linear EST 16-MAY-2004		Qy	1581	TGGGGTCTGGCCCCCAAATGCCTAACCCAGGACCTGGGAATTCTACTCATCCCCAA	1640
DEFINITION	17000532189001 GRN_ES Homo sapiens cDNA 5', mRNA sequence.			Db	459	TGGGGTCTGGCCCCCAAATGCCTAACCCAGGACCTGGGAATTCTACTCATCCCCAA	518
ACCESSION	CN373214			Qy	1641	GATAATTCCAATGCTGTTACCCAAAGTTAGGGTGTGAAGGAAGGTA	1688
VERSION	CN373214.1	GI:47373148		Db	519	GATAATTCCAATGCTGTTACCCAAAGTTAGGGTGTGAAGGAAGGTA	566
KEYWORDS							
SOURCE							
ORGANISM	Homo sapiens (human)						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 581)						
AUTHORS	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.						
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation						
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)						
COMMENT	Contact: Brandenberger R						
	Regeneron Medicine						
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	/mol_type="mRNA"						
	/db_xref="taxon:9606"						
	/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"						
	/clone_lib="GRN_ES"						
	/notes="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"						
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	Best Local Similarity 100.0%; Pred. No. 3.6e-272; Mismatches 0; Indels 0; Gaps 0;						
	Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1161	CCGGTTCCATCTTAAGCCCTTAACCTGAGCTCGTTAATGTAGCTCTGGCATG	1220	Qy	1341	TTTGTGATCCACCCCCCTTACCTTATCAGGATGTTGGCTGTTGGCTCTCTGTG	1400
Db	39	CCTGGTTCCATCTTAAGCCCTTAACCTGAGCTCGTTAATGTAGCTCTGGCATG	98	Db	219	TTTGTGATCCACCCCCCTTACCTTATCAGGATGTTGGCTGTTGGCTCTCTGTG	278
Qy	1221	GGAGTTCTAGGATGAAACACTCCTCATGGGATTGAACATATGAGTTATTGTAGG	1280	Qy	1401	CCATCACAGAGACAGGCAATTAACTTAACTTAACTTAACTTAAAGTGAAGGGA	1460
Db	99	GGAGTTCTAGGATGAAACACTCCTCATGGGATTGAACATATGAGTTATTGTAGG	158	Db	279	CCATCACAGAGACAGGCAATTAACTTAACTTAACTTAAAGTGAAGGGA	338
Qy	1281	GGAAGAGTCCTAGGGCACACACAAGAACAGGTCCTCAGGCCACAGCACTGTCTT	1340	Qy	1461	ATCCATGCTAGCTTCTGTGTTGGTCTAATATTGGTAGGGGGATCCCAA	1520
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				Qy	1521	CAATCAGAGACAGGCAATTAACTTAACTTAACTTAACTTAAAGTGAAGGGA	1580
				Db	399	CAATCAGGTCCTGAGATAGCTGCTCATGGGTGATCATGCCAGAATCTCTTCTCC	458
				Qy	1581	TGGGGTCTGGCCCCCAAATGCCTAACCCAGGACCTGGGAATTCTACTCATCCCCAA	1640
				Db	459	TGGGGTCTGGCCCCCAAATGCCTAACCCAGGACCTGGGAATTCTACTCATCCCCAA	518
				Qy	1641	GATAATTCCAATGCTGTTACCCAAAGTTAGGGTGTGAAGGAAGGTA	1688
				Db	519	GATAATTCCAATGCTGTTACCCAAAGTTAGGGTGTGAAGGAAGGTA	566
RESULT 12							
LOCUS	BG469586	589 bp mRNA linear EST 21-MAR-2001		REFERENCE	602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5', mRNA sequence.		
DEFINITION	BG469586			AUTHORS	1 (bases 1 to 589)		
ACCESSION	BG469586			TITLE	NIH-MGC http://mgc.nci.nih.gov/		
VERSION	BG469586.1	GI:13401861		KEYWORDS	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Contact: Robert Strausberg, Ph.D.			SOURCE	Unpublished (1999)		
	Email: cgabs-r@mail.nih.gov			ORGANISM	Homo sapiens		
	Tissue Procurement: ATCC						
	CDNA Library Preparation: Ling Hong/Rubin Laboratory						
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)						
	DNA Sequencing by: NIH Intramural Sequencing Center						
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov						
	Plate: LILM1460 row: k column: 05						
	High quality sequence stop: 587.						
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	/lab_host="DH10B (phage-resistant)"						
	/clone_lib="NIH_MGC_15"						
	/note="Organ: colon; Vector: pOTB7; Site 1: xhoI; Site_2:						
	EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'						
	adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in						
	the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"						
	ORIGIN						

Query Match		Score	491;	DB	4;	Length	589;
Best Local Similarity	100.0%	Pred.	No.	3.1e-252;	Mismatches	0;	Indels 0; Gaps 0;
Matches	491;	Conservative	0;	Mismatches	0;	Indels 0;	Gaps 0;
ACCGAGTTGAACTATGAAAGTTATTGTAGCTCTGGCATGGAGTTCTAGGATGAAACACTCCTCCAT	1249						
2 CTGCAGCTCGTTAATGTAGCTCTGGCATGGAGTTCTAGGATGAAACACTCCTCCAT	61						
GGGATTGTTGAACATATGAAAGTTATTGTAGCTCTGGCATGGAGTTCTAGGATGAAACACTCCTCCAT	1250						
62 GGGATTGTTGAACATATGAAAGTTATTGTAGCTCTGGCATGGAGTTCTAGGATGAAACACTCCTCCAT	61						
ACCGAGTTCCCTCAGCCCCACAGCACTGCTCTGGCATGGGGAAAGAGTCTTAGGGCAACACACAAGA	1309						
1310 ACCAGGTTCCCTCAGCCCCACAGCACTGCTCTGGCATGGGGAAAGAGTCTTAGGGCAACACACAAGA	121						
122 ACCAGGTTCCCTCAGCCCCACAGCACTGCTCTGGCATGGGGAAAGAGTCTTAGGGCAACACACAAGA	181						
ATCAGGATGGCCCTGTTGGCTCTCTGTGTCATCACAGAGACACAGGATTAAAT	1429						
182 ATCAGGATGGCCCTGTTGGCTCTCTGTGTCATCACAGAGACACAGGATTAAAT	241						
TTAACTTATTAAACAAAGTAGAAAGGAATCCATTGCTAGCTTTCTGTGTTGGTT	1489						
242 TAACTTATTAAACAAAGTAGAAAGGAATCCATTGCTAGCTTTCTGTGTTGGTT	301						
CTAATATTGGGTAGGGTGGGGATCCCCAACATCAGGTCCTGGAGATAGCTGGTCAT	361						
302 TGGGCTGATCATTGCCAGAACACACAAAGAACCCAGGTCCCTCAGGTCCTGGTCAT	1549						
1550 TGGGCTGATCATTGCCAGAACACACAAAGAACCCAGGTCCCTCAGGTCCTGGTCAT	1609						
362 TGGGCTGATCATTGCCAGAACACACAAAGAACCCAGGTCCCTCAGGTCCTGGTCAT	421						
CAGGACCTTGGAAATTCTACTCATCCAAATGATAATTCCAAATGCTGTACCAAGGT	1669						
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AGGGTGTGAA 1680							
482 AGGGTGTGAA 492							
ORIGIN							
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Best Local Similarity	100.0%	Pred.	No.	1.4e-243;	Mismatches	0;	Indels 0; Gaps 0;
Matches	475;	Conservative	0;	Mismatches	0;	Indels 0;	Gaps 0;
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1 1 GAGTCTGAGGGCAACACACAAAGAACCCAGGTCCCTCAGGCCACAGCACTGTCCTTG	60						
CTGATCCACCCCTCTACCTTTACGATGTTGGCTGTTGGCTCTGTGTCAT	120						
1345 CTGATCCACCCCTCTACCTTTACGATGTTGGCTGTTGGCTCTGTGTCAT	1404						
61 CTGATCCACCCCTCTACCTTTACGATGTTGGCTGTTGGCTCTGTGTCAT	120						
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1405 CACAGAGACACAGGATTAAATTAACCTATTAACTTAACTTAACTTAACT	1524						
181 ATTGCTAGCTTCTGTGTTGGTGTCAATTGGTAGGTGGGGATCCCAACAT	240						
1525 CAGGCCCCCTGAGATAGCTGGCATGGGTGATCATGCCAGAACCTCTCTCTGG	1584						
241 CAGGCCCCCTGAGATAGCTGGCATGGGTGATCATGCCAGAACCTCTCTGG	300						
GTCTGGCCCCCAAATGCCAACCCAGGACCTGGAAATTCTACTCATCCAAATGATA	1644						
301 GTCTGGCCCCCAAATGCCAACCCAGGACCTGGAAATTCTACTCATCCAAATGATA	360						
ATTCCTAAATGCTGTACCAAGGTAGGGTAGGGGTGGGCTTCAG	1704						
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BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
ACCESSION	5', mRNA sequence.						
VERSION	BM914562						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
RESULT 14							
BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
ACCESSION	5', mRNA sequence.						
VERSION	BM914562						
KEYWORDS	EST.						
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ORGANISM	Homo sapiens						
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LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
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VERSION	BM914562						
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ORGANISM	Homo sapiens						
RESULT 14							
BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
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LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
ACCESSION	5', mRNA sequence.						
VERSION	BM914562						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
RESULT 14							
BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
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VERSION	BM914562						
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ORGANISM	Homo sapiens						
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LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
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VERSION	BM914562						
KEYWORDS	EST.						
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ORGANISM	Homo sapiens						
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BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			
ACCESSION	5', mRNA sequence.						
VERSION	BM914562						
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ORGANISM	Homo sapiens						
RESULT 14							
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LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
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ACCESSION	5', mRNA sequence.						
VERSION	BM914562						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
RESULT 14							
BM914562							
LOCUS	BM914562	1060 bp	mRNA	linear	EST	12-MAR-2002	
DEFINITION	AGENCOURT_6615475 NIH_MGC_113	Homo sapiens	cdNA clone	IMAGE:5480245			

FEATURES	ORGANISM	Homo sapiens	
source	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ACCESSION	AUTHORS	1 (bases 1 to 515)	
VERSION	COMMENT	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelf, U., Schneider, D. and Korn, B.	
SOURCE	JOURNAL	Human Unigeneset - RZPD3	
RESULT 15	COMMENT	Unpublished (2003)	
BX098291	CONTACT	Contact: Ina Rolfs	
LOCUS	RZPD	Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
DEFINITION	RZPD	In Neuenheimer Feld 580, D-69120 Heidelberg, Germany	
IMAGP998P04693	RZPDLIB	RZPD; IMAGP998P04693.	
BX098291	Human Unigeneset	RZPDLIB; I.M.A.G.E. cDNA Clone Collection;	
BX098291.1	RZPD3	Human Unigeneset - RZPD3 (RZPDLIB No. 972)	
EST.	http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972	http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972	
Homo sapiens (human)	CONTACT	Contact: Ina Rolfs	
ORGIN	ORGANISM	Homo sapiens	
Query Match	Best Local Similarity	22.0%; Score 474; DB 5; Length 1060;	
Matches 474; Conservatve	Pred. No.	4.7e-243;	
0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Qy	AUTHORS	1 (bases 1 to 515)	
Db	COMMENT	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelf, U., Schneider, D. and Korn, B.	
360	TITLE	Tissue Procurement: Dr. Mark Watson	
CTGGAGGTGCTAGCAGTGGAGCACGCCCTAGCTG 419	JOURNAL	CDNA Library Preparation: Rubin Laboratory	
1 CTGGAGGTGCTAGCAGTGGAGCACGCCCTAGCTG 60	REFERENCE	DNA Sequencing by: Agencourt Bioscience Corporation	
Qy	ACCESSION	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
420	VERSION	http://image.llnl.gov	
GAGCTCCCTCCCTAATGGACACGTGGCTGGAGGCAGTGGCTGCTCCCACCTCCAC 479	SOURCE	Plate: LLCM2002 row: m column: 14	
61	COMMENT	High quality sequence stop: 485.	
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181	0; Mismatches 0; Indels 0; Gaps 0;	/clone_lib="NIH MGC 113"	
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ORGIN	ORGANISM	Homo sapiens	
Query Match	Best Local Similarity	22.0%; Score 474; DB 5; Length 1060;	
Matches 474; Conservatve	Pred. No.	4.7e-243;	
0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Qy	AUTHORS	1 (bases 1 to 515)	
Db	COMMENT	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelf, U., Schneider, D. and Korn, B.	
360	TITLE	Tissue Procurement: Dr. Mark Watson	
CTGGAGGTGCTAGCAGTGGAGCACGCCCTAGCTG 419	JOURNAL	CDNA Library Preparation: Rubin Laboratory	
1 CTGGAGGTGCTAGCAGTGGAGCACGCCCTAGCTG 60	REFERENCE	DNA Sequencing by: Agencourt Bioscience Corporation	
Qy	ACCESSION	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
420	VERSION	http://image.llnl.gov	
GAGCTCCCTCCCTAATGGACACGTGGCTGGAGGCAGTGGCTGCTCCCACCTCCAC 479	SOURCE	Plate: LLCM2002 row: m column: 14	
61	COMMENT	High quality sequence stop: 485.	
GAGCTCCCTCCCTAATGGACACGTGGCTGGAGGCAGTGGCTGCTCCCACCTCCAC 120	FEATURES	Location/Qualifiers	
480	source	1. .515	
CCGCCTCTGGGGCTCTGCCCTGTGATGTCTCCGTACGTTGGTGTAGCCCTGGATAGTG 539	ORGIN	/organism="Homo sapiens"	
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540	Matches 474; Conservatve	/clone="IMAGE:998P04693 ; IMAGE:308595"	
CCGAGGCCAGGGTGGTCCGGGCACTGCTGGACCTGCCATCCTGGATAGTG 599	Pred. No.	/lab_host="DH10B (ampicillin resistant)"	
181	0; Mismatches 0; Indels 0; Gaps 0;	/clone_lib="Soares_fetal_lung_NBHL19W"	
CCGAGGCCAGGGTGGTCCGGGCACTGCTGGACCTGCCATCCTGGATAGTG 240	REFERENCE	/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' -TGT TACCA ATCTG AAG TGG AGG GCG CCA ATTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."	
ORGIN	ORGANISM	Homo sapiens	
Query Match	Best Local Similarity	21.8%; Score 470; DB 5; Length 515;	
Matches 470; Conservatve	Pred. No.	6.4e-241;	
0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Qy	AUTHORS	1 (bases 1 to 515)	
Db	COMMENT	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelf, U., Schneider, D. and Korn, B.	
660	TITLE	Tissue Procurement: Dr. Mark Watson	
AGTCTGTCACTGCCTATATGGTCTGCCGCCAGGCCTGGCTGGCTGCCATTACTTG 719	JOURNAL	CDNA Library Preparation: Rubin Laboratory	
301	ACGTCTGTCACTGCCTATATGGTCTGCCATTACTCATCCCAATTGATAATTCCA 360	REFERENCE	DNA Sequencing by: Agencourt Bioscience Corporation
720	ACGTCTGTCACTGCCTATATGGTCTGCCATTACTCATCCCAATTGATAATTCCA 779	ACCESSION	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
361	CTACACAGGTAGTTGACAAGAGCGACTTGGCCAATACTCAGGTAGAAACTCCA 420	VERSION	http://image.llnl.gov
780	GCACATGGGGTGGAGGGCCTGCCTCACTGGGCCAGCTCCCGCTCTGTGTA 833	SOURCE	Plate: LLCM2002 row: m column: 14
421	421 GCACATGGGGTGGAGGGCCTGCCTCACTGGGCCAGCTCCCGCTCTGTGTA 474	COMMENT	High quality sequence stop: 485.
RESULT 15	FEATURES	Location/Qualifiers	
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LOCUS	REFERENCE	BX098291 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone	
DEFINITION	ACCESSION	IMAGP998P04693 ; IMAGE:308595, mRNA sequence.	
ACCESSION	VERSION	BX098291	
VERSION	SOURCE	BX098291.1 GI:27843586	
SOURCE	EST.		
Homo sapiens (human)	COMMENT		

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Db	394	TCTCACACAGAAACTCAGGAGCACCCCTGCTGAGCTAAGGGAGGTCTATCTCTCAGG	453
QY	2025	GGGGGTTAAGTGCCTTGCAATTATGTCGTTATTATTAGGGGG	2074
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Search completed: February 8, 2005, 21:26:58
Job time : 7013.66 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 09:49:12 ; Search time 9229.62 Seconds
 (without alignments)
 11250.684 Million cell updates/sec

Title: US-09-841-894A-15

Perfect score: 2143

Sequence: 1 ACCAGGGCGTGCAGAGCTTCTGGCTCTGGCTCTCTCTGG 2143

Scoring table: OLIGO_NUC* Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

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9: gb_pr:*

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11: gb_sts:*

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13: gb_un:*

14: gb_v1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

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14: gb_v1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AR112294

AR112294 Locus

AR112294 Definition Sequence 15 from patent US 6130043.

AR112294 Accession AR112294

AR112294.1 Version

GT:14092194

Keywords

Source Unknown

Organism Unclassified

Reference 1 (bases 1 to 2143)

Authors Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hedges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.

Reagents and methods useful for detecting diseases of the prostate

Title Patent: US 6130043-A 15-10-OCT-2000;

Journal

Features Location/Qualifiers

Source 1. .2143

/organism="unknown"

/mol_type="unassigned" DNA"

ORIGIN

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4 1916 89.4 2904 6 AR278710 AR278710 Sequence

5 1916 89.4 2904 6 AR400442 AR400442 Sequence

6 1916 89.4 2904 6 AR405709 AR405709 Sequence

7 1916 89.4 2904 6 AR564089 AR564089 Sequence

8 1916 89.4 2904 6 AX200994 AX200994 Sequence

9 1916 89.4 2904 6 AX267729 AX267729 Sequence

10 1900 88.7 3320 6 AX327336 AX327336 Sequence

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22 1764 82.3 4894 6 AX257728 AX257728 Sequence

23 1739 81.1 3410 6 BD242022 BD242022 Compounds

24 1739 81.1 3410 6 AR237205 AR237205 Sequence

25 1739 81.1 3410 6 AR278229 AR278229 Sequence

26 1739 81.1 3410 6 AR366925 AR366925 Sequence

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28 1739 81.1 3410 6 AR392326 AR392326 Sequence

29 1739 81.1 3410 6 AR399961 AR399961 Sequence

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34 1739 81.1 3410 6 AX140620 AX140620 Sequence

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39 1739 81.1 3410 9 AY033593 AY033593 Homo Sapi

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41 1651 77.0 6976 6 AR400444 AR400444 Sequence

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43 1651 77.0 6976 6 AR564091 AR564091 Sequence

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45 1651 77.0 6976 6 AX267731 AX267731 Sequence

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QY	541	GGGTGGTCCGGGGCATCTGCCCTGGGACCTGCCATCCTGGATAGTGCC	540	QY	1621	TCATCCCAAATGATAATTCCAATGCTTACCCAGGTTAACCAAGGTTAGGGTGTGAGGATAGTGCC	600
QY	601	TGTCCTCAGGTGGCCCATCCCTGTATGGGCTCATGCTCCAGCTCAGCTGTCA	600	Db	1621	TCATCCCAAATGATAATTCCAATGCTTACCCAGGTTAACCAAGGTTAGGGTGTGAGGATAGTGCC	600
QY	601	TGTCCTCAGGTGGCCCATCCCTGTATGGGCTCATGCTCCAGCTCAGCTGTCA	600	QY	1681	AGGGTGGGCTTCAGGTCTCAACGGCTTCCATAACCCACCCCTCTGGCCAGCCT	1740
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QY	841	CGGGCTGGCCGAGCTTCTGTGCTGCCAAAGTAATGTGGCTCTGTGCTGCCAACCTGT	840	QY	1921	ATCTCAGCCCCAGAGTATCTGTGCTGGAAATCTCACACAGAAACTCAGGACC	1980
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QY	961	TCTCTAGGGCTGCCAGTCTGCTGAGCTGGAGGCTTCCAAAGGGGTTCACTGCTGACTTACAGGG	1020	Db	1981	CCCTGCTGAGCTTCTGAGGAGGTCTTATCTCTAGGGGAATCTCACACAGAAACTCAGGACC	2040
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QY	1021	AGGCCAGAAGGGCTCCATGCACTGGAAATGGGACTCTGCAGGGATTACCCAGGG	1080	QY	2101	TAATGTTATGGTACGAAATTAAAGGCTTCTTATATGTTA	2143
QY	1081	GGTTAACAGCTCCAGCTAGTGAGACACACCTAGAGAACGGGTTGGGAGCTGAAT	1140	Db	2101	TAATGTTATGGTACGAAATTAAAGGCTTCTTATATGTTA	2143
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LOCUS	AR112295	AR112295	AR112295	DEFINITION	Sequence 16 from patent US 6130043.	2152 bp	DNA
ACCESSION	AR112295	AR112295	AR112295	VERSION	AR112295.1	GI:14092195	Linear
KEYWORDS				SOURCE	Unknown.	PAT 16-MAY-2001	
ORGANISM	Unclassified.						
REFERENCE	1			AUTHORS	Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.		
JOURNAL	1261	TTATTTGAGGGAAAGAGTCCTGAGGGCAACACACAAGAACCCAGGTCCCTCAGCCCCAC	1320	REAGENTS	Reagents and methods useful for detecting diseases of the prostate		
FEATURES	1261	TTATTTGAGGGAAAGAGTCCTGAGGGCAACACACAAGAACCCAGGTCCCTCAGCCCCAC	1320	PATENT	US 6130043-A 16-OCT-2000;		
1321	AGCACTGTCCTTGTGATCCACCCCTCTTACCTTTATCAGGATGGCCTGTTGG	1380	LOCATION	Location/Qualifiers			

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Best	Local Similarity	99.9%	Pred. No. 0;
Matches	2142; Conservative	0;	Mismatches 1;
Matches	2142; Conservative	0;	Mismatches 1;
Indels	1;	1;	Gaps 1;
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Qy	1140	TAAACTCAGTCACCTGGTTCCCATCTTAAGCCCTTAACCTGCAGCTTGTTAATGT	1199
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Qy	1200	AGCTCTGGAGTTCTAGGATGAAACACTCCTCCATGGATTGAAACATATGAA	1259
Db	1209	AGCTCTGGAGTTCTAGGATGAAACACTCCTCCATGGATTGAAACATATGAA	1268
Qy	1260	GTTATTGGAGAGTCTTAGGATGAAACACTCCTCCATGGATTGAAACATATGAA	1319
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Qy	1320	CAGCCTACCGGAGAACGGGACTGGAGCT 300	1379
Db	1329	CAGCCTACCGGAGAACGGGACTGGAGCT 300	1388
Qy	1380	GTCCTCTGTCTTGTGATCCACCCCTTACCTTATCAGGATGTGGCTGTG	1388
Db	1389	GTCCTCTGTCTTGTGATCCACCCCTTACCTTATCAGGATGTGGCTGTG	1388
Qy	1440	AAGTAGAAGGAATCCAATGCTAGCTTCTGTGGTGGCTAATATTAGGGTAGGTG	1439
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Qy	1560	ATCTCTCTCTGGGCTCTGGCTTAATGCCCTAACCCAGGCCATGGCTGATCATGCCAGA	1619
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Qy	1620	CTCATCCCCAATGATAATCCAAATGCTGTACCCAAGGTAGGGTGTGAAGGAAGGTAA	1679
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Qy	1680	GAGGGTGGGCTTCAGGTCTAACGGCTTCCCTAACCCCTCTCTGGCCAGGCC	1739
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Qy	1920	CATCTCAGCCCCAAGATACTGTGTGCTTCAAGGGGTTAAGTGCCTTGCAAT	1979
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Qy	1980	CCCTGCTGAGGTCTAGGAGGCTTCTCTCAAGGGGTTAAGTGCCTTGCAAT	2039
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ACCESSION	BC050416		
VERSION	BC050416.2	GI:34194585	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo. 1 (bases 1 to 3306)		
REFERENCE	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schulter, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
JOURNAL	1247932		
PUBMED	2 (bases 1 to 3306)		
REFERENCE	Strausberg, R.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov On Aug 25, 2003 this sequence version replaced gi:29791944. Contact: MGC help desk Email: cgaps-r@mail.nih.gov		
REMARK	CDNA Library Preparation: Dr. James R. Lupski Tissue Procurement: Dr. James R. Lupski DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu (Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.)		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: http://image.llnl.gov Series: IRAK Plate: 98 Row: n Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14916436. Location/Qualifiers 1. .3306 /organism="Homo sapiens" /moltype="mRNA"		

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Db	993	GCTTCAGCCGCCCCCTACCGGGTCAACCTTCTAGCCCTCAGATCTGCCTACACTG	1052	Qy	1376	GTTGGTCTTCTGTGTCATCACAGAGACAGGATTAATTAATTATT	1435
Qy	297	GCTTCCTCTACCAACGGAGAACAGGTTCTTGCCAAATACCGAGGAGACTGGA	356	Db	2133	GTTGGTCTTCTGTGTCATCACAGAGACAGGATTAATTAATTATT	2192
Db	1053	GCTTCCTCTACCAACGGAGAACAGGTTCTTGCCAAATACCGAGGAGACTGGA	1112	Qy	1436	AACAAAGTAGAGGAATCCATGCTAGCTTCTGTGTCATATTGGTAG	1495
Qy	357	GGTGCCTAGCACTGAGGAGACAGCAGCTGATGACCACTGGAGGAGCT	416	Db	1113	GGTGCCTAGCACTGAGGAGACAGCAGCTGATGACCACTGGAGGAGCT	1172
Db	1173	CCCTCCCTAATGGACACAGTGGCTGAGGAGCTCCACCCGG	476	Qy	1496	GTTGGGGATCCCAACATCAGTGGGCTGCTCCAGGCCTAACCTCACCGG	1555
Db	1233	CTCTGGGGGCTCTACCTGTGATGTCCTGGAGGAGCTGGCTG	1232	Db	2193	AACAAAGTAGAGGAATCCATGCTAGCTTCTGTGTCATATTGGTAG	2252
Qy	417	CTCTGGGGGCTCTACCTGTGATGTCCTGGAGGAGCTGGCTG	1232	Qy	1556	CAGAATCTCTCTGGGCTGGGCACTGCTGGACATCCACCCGG	536
Qy	477	CTCTGGGGGCTCTACCTGTGATGTCCTGGAGGAGCTGGCTG	1232	Db	2253	GTTGGGGATCCCAACATCAGTGGGCTGCTCCAGGCCTAACCTCACCGG	1292
Db	1293	GCAGGGTGTCCGGGGGATCTGCCTGGACCTGTC	1352	Qy	1556	CAGAATCTCTCTGGGCTGGGCACTGCTGGACATCCACCCGG	536
Qy	597	CTGCTGCCAGGTGGCCATCTGCCTGGACATCTGCCTGGACCTGTC	656	Db	2313	CAGAATCTCTCTGGGCTGGGGGAAATGCTAACCCAGGACCTGGGAAT	2312
Db	1353	CTGCTGCCAGGTGGGGGATCTGCCTGGACATCTGCCTGGACCTGTC	1412	Qy	1616	TCTACTCATCCCATAATGGGTCTGGCCATTACTTGCTA	716
Qy	657	GTCACTGCCATATGGTCTGGCTCAGGCTGGCTGGCTGGACATCTGCCTGGACCTGTC	716	Db	2373	TCTACTCATCCCATAATGGGTCTGGGGTAGGGTGTGAGGAA	2432
Db	1413	GTCACTGCCATATGGTCTGGCCATTACTTGCTA	1472	Qy	1676	GGTAGAGGGGGCTCAGGTCTCAACGGCTCCTAACCCAGGTAGGTGTC	1735
Qy	717	CAGGTAGTATTGACAAGAGGACTGGCAAACTCAGCGTAGAAACTCCAGCA	776	Db	2433	GGTAGAGGGGGCTTCAGGTCTCAACGGCTCCTAACCCAGGTAGGTGTC	2492
Db	1473	CAGGTAGTATTGACAAGAGGACTGGCTGGCCAAATCTAGCCATCCAGCA	1532	Qy	1736	ACTGCCAAATTCCTACCCCAACTTCCCTAACCCCAACTTCCCACCGAGC	1795
Qy	777	TTGGGGTGAAGGGCTGCTCACTGGTCCACGCTCCCCTGTAGCCCCATGGG	836	Db	2553	ACTGCCAAATTCCTACCCCAACTTCCCTACTCTCTAGACTGGGTG	2552
Db	1533	TTGGGGTGAAGGGCTGCTCACTGGTCCACGCTCCCAGCTCCCCCTGTAG	1592	Qy	1856	CACAAACCTGTTGGAGCTACTGCAGGACAGACAACAGCTTCCCACCGCT	1855
Qy	837	CTGCGGGCTGGCCCAAGTTCTGTGTCGCAAACTAATGGCTCTGTCACC	896	Db	2613	CACAAACCTGTTGGAGCTACTGCAGGACAGACAACAGCTTCCCACCGCT	2672
Db	1593	CTGCGGGCTGGCCCAAGTTCTGTGTCGCAAACTAATGGCTCTGTCACC	1652	Qy	1916	TGTCCATCTCAGCCCCAGAGTATATCTGTGCTGGGAACTCAGAGGA	1975
Qy	897	CTGTGCTGCTGAGGTGCTAGCTGACAGCTGGGGCTGGGGCTCTCTCTC	956	Db	2673	TGTCCATCTCAGCCCCAGAGTATATCTGTGCTGGGAACTCAGAGGA	2732
Db	1653	CTGTGCTGCTGAGGTGCTAGCTGACAGCTGGGGCTGGGGCTCTCTCTC	1712	Qy	1976	GCACCCCTGCTGAGCTAAGGGAGGTCTATCTCTAGGGGGTTAAGTGGCTTG	2035
Qy	957	CCAGTCTCTAGGGCTGCTGACTGGAGGCTTCAAGGGGTTCAAGGGGTT	1016	Db	2733	GCACCCCTGCTGAGCTAAGGGAGGTCTATCTCTAGGGGGTTAAGTGGCTTG	2792
Db	1713	CCAGTCTCTAGGGCTGCTGACTGGAGGCTTCAAGGGGTTCAAGGGGTT	1772	Qy	2036	CAATAATGTCCTTATTTAGGGGGTCAATTTATCTGTAAAGTGAGCAATCA	2095
Qy	1017	AGGGAGGCCAGAAGGGCTCATGGATGC-GGGACTCTGCAGGTGATTACCCAG	1075	Db	2793	CAATAATGTCCTTATTTAGGGGGTCAATTTATCTGTAAAGTGAGCAATCA	2852
Db	1773	AGGGAGGCCAGAAGGGCTCATGGATGC-GGGACTCTGCAGGTGATTACCCAG	1832	Qy	2096	GAGTAAATGTTATGGTGAACAAATTAAAGGTTCTTATAGTTA	2143
Qy	1076	GCTCAGGGTTAACAGCTAACCTCTAGTTGAGACACACTAGAGAAGGGTTGGAGC	1135	Db	2853	GAGTAAATGTTATGGTGAACAAATTAAAGGTTCTTATAGTTA	2300
Db	1833	GCTCAGGGTTAACAGCTAACCTCTAGTTGAGACACACTAGAGAAGGGTTGGAGC	1892	RESULT 5			
Qy	1136	TGAAATAACTCACTGGTTCACTCTAACCTGAGGAGACTAGAGAAGGGTTGGAGC	1195	AR40442			
Db	1893	TGAAATAACTCACTGGTTCACTCTAACCTGAGGAGACTAGAGAAGGGTTGGAGC	1952	LOCUS	AR40442		
Qy	1196	ATGTAGCTCTGCTGGAGTTCTAGGATGAAACACTCCCATGGGATTGACATAT	1255	DEFINITION	Sequence 703 from patent US 6620922.	2904 bp	DNA
Db	1953	ATGTAGCTCTGCTGGAGTTCTAGGATGAAACACTCCCATGGGATTGACATAT	2012	ACCESSION	AR40442		Linear
Qy	1256	GAAGTTATTGTTAGGGAGACTGGCTCTGAGGGCAACACACAGGTCCTCAG	1315	VERSION	AR40442.1	GI:40143818	PAT 18-DEC-2003
Db	2013	GAAGTTATTGTTAGGGAGACTGGCTCTGAGGGCAACACACAGGTCCTCAG	2072	KEYWORDS			
Qy			SOURCE				
			ORGANISM				
REFERENCE			Unknown.				
			Unclassified.				
			1 (bases 1 to 2904)				
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.						

Db	2793	CATAATGTCGTCTTATTAGGGGGTGAATTACTGTAAGTGACATCA	2852	Db	1353	CTGCTGCCCCAAGTGGCCCATCCCTGTTATGGCTCCATTGTCAGCTCAGCCAGTCT	1412
Qy	2096	GGTATAATGTTTATGGTACAAATAATTAAAGGCTTCTTATATGTTA	2143	Qy	657	GTCACTGCCTATATGGTCTGCGCGAGGCCTGGCTGGCTGCCTACTTTGCTACA	716
Db	2853	GGTATAATGTTTATGGTACAAATAATTAAAGGCTTCTTATATGTTA	2900	Db	1413	GTCACTGCCTATATGGTCTGCGCGAGGCCTGGCTGGCTGCCTACTTTGCTACA	1472
Qy				Qy	717	CAGGTAGTATTGACAAGAGGACTTGGCCAAATACTCAGCTAGAAAATTCCAGCACA	776
RESULT 6				Db	1473	CAGGTAGTATTGACAAGAGGACTTGGCCAAATACTCAGCTAGAAAATTCCAGCACA	1532
AR405709		AR405709	Sequence 703 from patent US 6630305.	Qy	837	CTGCCGGCTGGCCAGTTCTGTGCTGCCAAAGTAATGTTGCTCTGTGCTGCCAGCACA	896
LOCUS		ACCESSION	2904 bp DNA	Db	1533	TTGGGGAGGGCTGCCTACTGGGTCAGCTGGCTCCAGCTCCCTGTTAGCCCCATGGG	1592
DEFINITION		VERSION	linear	Qy	897	CTGTGCTGCTGAGGTGGCTACTGGGAGCTCCAGCTGGGCTGGCTCCCTCTCC	956
KEYWORDS			PAT 18-DEC-2003	Db	1653	CTGTGCTGCTGAGGTGGCTAGTGCACAGCTGGGCTGGCTCCCTCTCC	1712
SOURCE		ORGANISM	Unknown.	Qy	957	CCAGTCTCTAGGCTGCTGACTGGAGGCCTCCAAAGGGGTTCACTGGTAACTTAC	1016
REFERENCE		AUTHORS	Unclassified. 1 (bases 1 to 2904)	Db	1713	CCAGTCTCTAGGCTGCTGACTGGAGGCCTCCAAAGGGGTTCACTGGTAACTTAC	1772
		Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kilos,M.D., Fanger,G.R., Retter,M.W., Stoilk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.		Qy	1017	AGGGAGGCCAGAGGGCTCCATGCACTGGAAATGC-GGGACTCTGCAGGTGATTACCCAG	1075
TITLE		Compositions and methods for the therapy and diagnosis of prostate cancer		Db	1773	ACGGAGGCCAGAGGGCTCCATGCACTGGAAATGC-GGGACTCTGCAGGTGATTACCCAG	1832
JOURNAL		Patent: US 6630305-A 703 07-OCT-2003;		Qy	1076	GCTCAGGGTTAACAGCTAACAGCTCTCTAGTTGAGACACACACCTAGAGAAGGGTTGGGAGC	1135
FEATURES		source	1. 2904 /organism="unknown" /mol_type="genomic DNA"	Db	1833	GCTCAGGGTTAACAGCTAACAGCTCTCTAGTTGAGACACACACCTAGAGAAGGGTTGGGAGC	1892
ORIGIN				Qy	1136	TGAATAACTCAGTCACCTGGTTCCCATCTTAAGCCCTTAACCTGCAAGCTTCGTTA	1195
Query Match	89.4%	Best Local Similarity	99.9%; Pred. No. 0;	Db	1893	TGAATAACTCAGTCACCTGGTTCCCATCTTAAGCCCTTAACCTGCAAGCTTCGTTA	1952
Matches	2086;	Conservatory	0;	Qy	1196	ATGTACTCTGATGGGAGTTCTAGGATGAAACACTCCTCATGGGATTGAACTAT	1255
Qy	57	GGCGTTGGATGGGCAGCCCTGGGCTGTTCCCTGCAGTGCCTGCACATCTCCCTGGTCTCT	116	Db	1953	ATGTACTCTGATGGGAGTTCTAGGATGAAACACTCCTCATGGGATTGAACTAT	2012
Db	813	GGCGTTGGATGGGCAGCCCTGGGCTGTTCCCTGCAGTGCCTGCACATCTCCCTGGTCTCT	872	Qy	1256	GAAAGTTATTGTTAGGGAGAGCTGCTGAGGACACTGGA	1315
Qy	117	CTGGTCATGGACCGGCTGGTGCAGGGATTGGCACTCGGACTCGAGCAGTCTATTGCCAGTGT	176	Db	2013	GAAAGTTATTGTTAGGGAGAGCTGCTGAGGACACTGGA	2072
Db	873	CTGGTCATGGACCGGCTGGCAGGGATTGGCACTCGGACTCGAGCAGTCTATTGCCAGTGT	932	Qy	1316	CCCACAGCACTGCTTCTGATCCACCCCTTACCTTTATGAG3ATGTCGGCCT	1375
Qy	177	GCAGCTTCCCTGGGCTGGCCACATGCTCCAGGCTTACACACTG	236	Db	2073	CCCACAGCACTGCTTCTGATCCACCCCTTACCTTTATGAG3ATGTCGGCCT	2132
Db	933	GCAGCTTCCCTGGGCTGGCCACATGCTCCAGGCTTACACACTG	992	Qy	1376	GTGGGRCCTCTGTGCCCCATCACAGAGACACAGGATTAATTTAATTATT	1435
Qy	237	GCTTCAGGCCCTCACGGGTTCACCTCTCAGGCTTACACACTG	296	Db	2133	GTGGGCTCTCTGTGCCCCATCACAGAGACACAGGATTAATTTAATTATT	2192
Db	993	GCTTCAGGCCCTCACGGGTTCACCTCTCAGGCTTACACACTG	952	Qy	1436	AACAACTAGAAGGAATCCATTGCTAGCTTCTGTGTTGTTCTAATTGAG	1495
Qy	297	GCTCCCTCTACCAACGGGAGAACAGGGTTCTGCCAATACGGGACACTGGA	356	Db	2193	AACAACTAGAAGGAATCCATTGCTAGCTTCTGTGTTGTTCTAATTGAG	2252
Db	1053	GCTCCCTCTACCAACGGGAGAACAGGGTTCTGCCAATACGGGACACTGGA	992	Qy	1496	GGTGGGGATCCCCAACATCAGGCTCTGAGATAGCTGGTATGGCTGATCATG	1555
Qy	357	GGTGTAGCACTGAGGAACGGCTGTGATGACCGCTTCTGCCAGGGCTTAAGCCTGGAGCT	416	Db	2253	GGTGGGGATCCCCAACATCAGGCTCTGAGATAGCTGGCTGATCATG	2312
Db	1113	GGTGTAGCACTGAGGAACGGCTGTGATGACCGCTGAGCT	1052	Qy	1556	CAGAACTCTCTCTGGGCTGAGATAGCTGGTATGGCTGATCATG	1615
Qy	417	CCCTCCCTAATGGAACGGGGTCTGGAGGCACTGGCTGCTCCACCGG	476	Db	2313	CAGAACTCTCTGGGCTGAGATAGCTGGCTGATCATG	2372
Db	1173	CCCTCCCTAATGGAACGGGGTCTGGAGGCACTGGCTGCTCCACCGG	1232	Qy	1616	TCTACTCATCCAAATGATAATCCAATGCTGTTACCCAGGACCTGGAAAT	1675
Qy	477	CTCTGGGGGCTCTGCTGAGCTCTGGTACGGTCTGGCTGCTCCACCGG	536	Db	2373	TCTACTCATCCAAATGATAATCCAATGCTGTTACCCAGGTTAGGGCTTGAACGAA	2432
Db	1233	CTCTGGGGGCTCTGCTGAGCTCTGGTACGGTCTGGCTGCTCCACCGG	1232	Qy	1676	GGTAGAGGGGGCTCAGGCTCAAAGGCTTCCCTAACACCCCTCTCTTGCCCC	1735
Qy	537	GCCAGGGGTTCCGGGGGGGACATCTGCTGGACACTGCCATCTGGATAGTGCCCTC	596				
Db	1293	GCCAGGGGTTCCGGGGGGGACATCTGCTGGACACTGCCATCTGGATAGTGCCCTC	1352				
Qy	597	CTGCTGCCAGGGCCCCATCCCTGTTATGGCTCCATGTCAGGCCAGTCT	656				

		FEATURES	Location/Qualifiers
		source	1. .2904
QY	1376	GRGGGTCTCTGTCGCCATCACAGAGACAGGCATTAAATTAACTTATT	/organism="Homo sapiens"
Db	2133	GTTGGTCTCTGTGTCGCCATCACAGAGACAGGCATTAAATTAACTTATT	/mol_type="unassigned DNA"
QY	1436	ACAAAGTAGAACCGAATCCATTGCTAGCTTCTGTTGGTCTTAATTGGTAG	/db_xref="taxon:9606"
Db	2193	ACAAAGTAGAACCGAATCCATTGCTAGCTTCTGTTGGTCTTAATTGGTAG	
QY	1496	GCTGGGGATCCCCAACATCAGGCCCTGAGATAGCTGGTCATGGCTGATCATGG	
Db	2253	GTTGGGGATCCCCAACATCAGGCCCTGAGATAGCTGGTCATGGCTGATCATGG	
QY	1556	CAGAATCTTCTCTGGGCTGGCCCAAAATGCCAACCGGACCTTGAAT	
Db	2313	CAGAATCTTCTCTGGGCTGGCCCAAAATGCCAACCGGACCTTGAAT	
QY	1616	TCTACTCATCCAAATGATAATTCCAATGCTGTACCAAGGTAGGGTGTGAAGGA	
Db	2373	TCTACTCATCCAAATGATAATTCCAATGCTGTACCAAGGTAGGGTGTGAAGGA	
QY	1676	GGTAGAGGGGGCTCAGGTCTAACGGCTTCCCTAACACCCCTCTCTGGCC	
Db	2433	GGTAGAGGGGGCTCAGGTCTAACGGCTTCCCTAACACCCCTCTCTGGCC	
QY	1736	AGCCTGGTTCCCCCACTCCACTTCTACTCTCTTAGACTGGCTGATGAAGGC	
Db	2493	AGCCTGGTTCCCCCACTTCCACTTCTACTCTCTTAGACTGGCTGATGAAGGC	
QY	1796	ACTGCCAAATTCCCCCTACCCCAACTTCCCTACCCCAACTTCCCACAGCT	
Db	2553	ACTGCCAAATTCCCCCTACCCCAACTTCCCACAGCT	
QY	1856	CAACACCTTTGGAGCTACTGGAGGACAAAGCAGGAGCAGGTGTCTGCCCACAGCT	
Db	2613	CAACACCTTTGGAGCTACTGGAGGACAAAGCAGGAGCAGGTGTCTGCCCACAGCT	
QY	1916	TGTCATCTAGCCCCAGAGTATCTGTGCTGGGATCTCACACAGAAACTCAGGA	
Db	2673	TGTCATCTAGCCCCAGAGTATCTGTGCTGGGATCTCACACAGAAACTCAGGA	
QY	1976	GCACCCCTGCCTGAGCTAAGGGGCTTATCTCTAGGGGCTGAGGACAAAGTGGTTCCAGCT	
Db	2733	GCACCCCTGCCTGAGCTAAGGGGCTTATCTCTAGGGGCTGAGGACAAAGTGGTTCCAGCT	
QY	2036	CAATAATGTCGTTATTAGGGGTGAATTTATCTGAGGAGGTATCTCGCGTT	
Db	2793	CAATAATGTCGTTATTAGGGGTGAATTTATCTGAGGAGGTATCTCGCGTT	
QY	2096	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATATGTTA	
Db	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATATGTTA	
RESULT 8	AX200994	AX200994	2904 bp DNA linear PAT 29-AUG-2001
LOCUS	AX200994	Sequence 624 from Patent WO0151633.	
DEFINITION	AX200994		
ACCESSION	AX200994.1	GI:15390821	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens	Homo sapiens (human)	
ORGANISM	Homo sapiens		
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Ranger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 624 19-JUL-2001; CORIXA CORPORATION (US)		

Db	1713	CCAGTCTCTAGGGCTGCTGACTGAGGCCTTCAAGGGGTTCACTCTGGACTTATAC	1772	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1017	AGGGAGGCCAGAAGGGCTCCATGACTGGAATGC-GGGACTCTGCAGGGATTACCCAG	1075	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	1773	AGGGAGGCCAGAAGGGCTCCATGACTGGAATGGGGACTCTGCAGGGATTACCCAG	1832				
Qy	1076	GCTCAGGGTTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAACGGTTGGAGC	1135				
Db	1833	GCTCAGGGTTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAACGGTTGGAGC	1892	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1136	TGAATAACTCAGTCACCGGTTCCATCTCTAAGCCCTAACCTGCAGCTTGTAA	1195	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	1893	TGAATAACTCAGTCACCTGGTTCCATCTCTAAGCCCTAACCTGCAGCTTGTAA	1952				
Qy	1196	ATGTAGCTCTGCATGGAGTTCTAGGATGAAACACTCTCCATGGATTGACATAT	1255				
Db	1953	ATGTAGCTCTGCATGGAGTTCTAGGATGAAACACTCTCCATGGATTGACATAT	2012	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1256	GAAGTTATTGTTAGGGGAAGAGCTCTGAGGGCACACACAAGAACCGGTCCCTAG	1315	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	2013	GAAGTTATTGTTAGGGGAAGAGCTCTGAGGGCACACACAAGAACCGGTCCCTAG	2072				
Qy	1316	CCACAGCACTGCTTTTGCTGTATCCACCCCCCTTACCTTTATCAGGATGGCCT	1375				
Db	2073	CCACAGCACTGCTTTTGCTGTATCCACCCCCCTTACCTTTATCAGGATGGCCT	2132	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1376	GTTGGTCTCTGTGCATCACAGACAGGCAATTAAATTAACTTATTATT	1435	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	2133	GTTGGTCTCTGTGCATCACAGACAGGCAATTAACTTATTATT	2192				
Qy	1436	AACAAAGTAGAGGAAATCCATGCTAGTTCTGTGTGGTGTCTAATTGGTAG	1495				
Db	2193	AACAAAGTAGAGGAAATCCATGCTAGTTCTGTGTGGTGTCTAATTGGTAG	2252	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1496	GTTGGGATCCCCAACATCAGGCCCCCTGAGATAGCTGGCATGGCTGATCATGC	1555	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	2253	GTTGGGATCCCCAACATCAGGCCCCCTGAGATAGCTGGCATGGCTGATCATGC	2312				
Qy	1556	CAGAATCTCTCTGGGGCTGGCCCCAAATGCTAACCCAGGACTTGTAA	1615	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2313	CAGAATCTCTCTGGGGCTGGGGCTGGCCCCAAATGCTAACCCAGGACCTTGTAA	2372	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Qy	1616	TCTACTCATCCAAATGATAATTCCAATGCTGTACCCAGGTTAGGGTGTGAACGAA	1675	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2373	TCTACTCATCCAAATGATAATTCCAATGCTGTACCCAGGTTAGGGTGTGAAGGAA	2432	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Qy	1676	GCTAGAGGGTGGGCTTCAGGCTAACGGCTTCCAACCCCTCTCTGGCC	1735	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2433	GCTAGAGGGTGGGCTTCAGGCTAACGGCTTCCAACCCCTCTCTGGCC	2492	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Qy	1736	AGCCCTGGTCCCCCACTTCAACCCCTCTACTCTCTAGGACTGGGCTGATGAAGGC	1795	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2493	AGCCCTGGTCCCCCACTTCAACCCCTCTACTCTCTAGGACTGGGCTGATGAAGGC	2552	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Qy	1796	ACTGCCAAATTCCCTACCCCCAACCTTCCCTACCTCTAGGACTGGGCTGATGAAGGC	1855	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2553	ACTGCCAAATTCCCTACCCCCAACCTTCCCTACCTCTAGGACTGGGCTGATGAAGGC	2612	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2900
Qy	1856	CACAAACCTGTGGAGCTACTGCGAGGACAGAACAGTGGGTTCCAAGCCTT	1915	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2613	CACAAACCTGTGGAGCTACTGCGAGGACAGAACAGTGGGTTCCAAGCCTT	2672	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Qy	1916	TGTCCATCTAGCCCCAGAGTATCTGTGCTAACAGAACACTCAGGA	1975				
Db	2673	TGTCCATCTAGCCCCAGAGTATCTGTGCTAACAGAACACTCAGGA	2732	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Qy	1976	GCACCCCTGCTGAGCTAACGGAGCTTCTGAGGGGTTAAGTGCCTTG	2035	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900
Db	2733	GCACCCCTGCTGAGCTAACGGAGGTCTTCTCTAGGGGGTTAAGTGCCTTG	2792				
Qy	2036	CAATAATGTCGTTATTAGGGGTTAATTACTGTAAGTGACCAATCA	2095	Qy	2096	GAGTATAATGTTATGGTACAAATAAGGTTCTTATGTTA	2143
Db	2793	CAATAATGTCGTTATTAGGGGTTAATTACTGTAAGTGACCAATCA	2852	Qy	2853	GAGTATAATGTTATGGTACAAATAAGGCTTCTTATGTTA	2900

QY	597	CTGCTGTCCCAGGCTGCCCATCCCTGTTATGGCTCCATTGCCAGCTCAGCCAGTCT	656
Db	1353	CTGCTGTCCCAGGCTGCCCATCCCTGTTATGGCTCCATTGCCAGCTCAGCCAGTCT	1412
QY	657	GTCACTGCCTATATGGTGTCTGCCGAGGCTGGTCTGGTCTGGCTTACTTTGCTACA	716
Db	1413	GTCACTGCCTATATGGTGTCTGCCGAGGCTGGTCTGGTCTGGCTTACTTTGCTACA	1472
QY	717	CAGGTAGTATTGACAAGAGCGACTTGGCCAAACTCAGCGTAGAAACCTCCAGACA	776
Db	1473	CAGGTAGTATTGACAAGAGCGACTTGGCCAAACTCAGCGTAGAAACCTCCAGACA	1532
QY	777	TTGGGGGGAGGGCTGCTCACTGGTCCAGTTCTGTGCTGGCCAAACTCAGCGTAGAAACCTCCAGACA	836
Db	1533	TTGGGGGGAGGGCTGCTCACTGGTCCAGTTCTGTGCTGGCCAAACTCAGCGTAGAAACCTCCAGACA	1592
QY	837	CTGCCGGCTGCCGCCAGTTCTGTGCTGCCAAACTCAGCGTAGAAACCTCCAGACA	896
Db	1593	CTGCCGGCTGCCGCCAGTTCTGTGCTGCCAAACTCAGCGTAGAAACCTCCAGACA	1652
QY	897	CTGTCGCTCTGAGGTGCGTAGCTGCCACAGCTGGGCTCTCTCTGCCACC	956
Db	1653	CTGTCGCTCTGAGGTGCGTAGCTGCCACAGCTGGGCTCTCTCTGCCACC	1712
QY	957	CCAGTCTCTAGGGCTGCCGTGACTGGGCTTCAGTCTGGGACTTAC	1016
Db	1713	CCAGTCTCTAGGGCTGCCGTGACTGGGCTTCAGTCTGGGACTTAC	1772
QY	1017	AGGGAGGCCAGAAGGCTCCATGCCACTGGAAATGC-GGAACTCTGCAAGGTGATTAC	1075
Db	1773	AGGGAGGCCAGAAGGCTCCATGCCACTGGAAATGC-GGAACTCTGCAAGGTGATTAC	1832
QY	1076	GCTCACGGGTTACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGTTTGGGAGC	1135
Db	1833	GCTCACGGGTTACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGTTTGGGAGC	1892
QY	1136	TGAATAACTCAGTCACCTGGTTCCATCTTAAGCCCTTAACCTGCAGCTCGTTA	1195
Db	1893	TGAATAACTCAGTCACCTGGTTCCATCTTAAGCCCTTAACCTGCAGCTCGTTA	1952
QY	1196	ATGTAGCTCTGCATGGAGTTCTAGGATGAAACACTCCTCCATGGGATTGAAACATAT	1255
Db	1953	ATGTAGCTCTGCATGGAGTTCTAGGATGAAACACTCCTCCATGGGATTGAAACATAT	2012
QY	1256	GAAAGTTATTGAGGGAGAGTCTTAGGATGAAACACTCCTCCATGGGATTGAAACATAT	1315
Db	2013	GAAAGTTATTGAGGGAGAGTCTTAGGATGAAACACTCCTCCATGGGATTGAAACATAT	2072
QY	1316	CCCACGCACTGCTTTGCTGATCCACCCCCCTTACTTATCAGGATGTGGCT	1375
Db	2073	CCCACGCACTGCTTTGCTGATCCACCCCCCTTACTTATCAGGATGTGGCT	2132
QY	1376	GTGGGCTTCTGTGCCATCACAGACACAGGCAATTAAATTAACCTTT	1435
Db	2133	GTGGGCTTCTGTGCCATCACAGACACAGGCAATTAAATTAACCTTT	2192
QY	1436	AACAAAGTAGAAGGAATTCCATTGCTAGCTTCTGTGGTGTAAATTGGTAG	1495
Db	2193	AACAAAGTAGAAGGAATTCCATTGCTAGCTTCTGTGGTGTAAATTGGTAG	2252
QY	1496	GGTGGGGATCCCCAACATCAGGCCCCCTGAGATAGCTGGTCTGGCTGATCATGC	1555
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QY	1976	GCACCCCCCTGCCGTGAGCTAAGGGAGGTCTTATCTCTCACACAGAACTCAGGA	2792
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DEFINITION	Sequence 1 from Patent WO0181577.	3320 bp	DNA
ACCESSION	AX327336	AX327336.1	PAT 07-JAN-2002
VERSION	AX327336.1	GI:18097882	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W., Steinbrecher, R., van Heut, P.T. and Wu, J.		
TITLE	Dna encoding the prost 03 polypeptide		
JOURNAL	Patent: WO 0181577-A 1 01-NOV-2001; SCHERING AKTIENGESELLSCHAFT (DE)		
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Qy	61	TTCGGATGGGCAGCCTGGGCTGTCTGCAGTGCCTCATCTCCCTGTTCTCTCTGG								Qy
Db	1243	TTCGGATGGGCAGCCTGGGCTGTCTGCAGTGCCTCATCTCCCTGTTCTCTCTGG								Db
Qy	121	TCA TG GAC CCG CT GT G CAG G AT T C G G C A C T C G G C A G C A T T G G C A G								Qy
Db	1303	TCA TG GAC CCG CT GT G CAG G AT T C G G C A C T C G G C A G C A T T G G C A G								Db
Qy	181	CTT TCC CT GT G C G C T G C C A C T G C C T G T G C C A C A T G C C T G T G C C C A C A G T G T G G C C G T G G C A G								Qy
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Qy	241	CAGCCGCCTCACGGGTTCACCTTCTCAGCCCTGAGATCCTGCAGACACTGGCCT								Qy
Db	1423	CAGCCGCCTCACGGGTTCACCTTCTCAGCCCTGAGATCCTGCAGACACTGGCCT								Db
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Db	1483	CCCTCTACCAACGGGAGAACCTTCTCAGCCCTGAGATCCTGCAGACACTGGCCT								Db
Qy	361	CTAGCAGTGGAGACAGCTGTAGACCCAGCTCTGGAGGCTCC								Qy
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Qy	541	G G G T G G T C C G G G C A T C T G C C T G G A C T C G C C A T C T G G A T A G T G C C T C C T G C								Qy
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Qy	721	T A G T A T T G A C A A G G C A C T T G G C C A A T A T C T C A G C T G A A A A C T T C C A G C A C A T T G G								Qy
Db	1903	T A G T A T T G A C A A G G C A C T T G G C C A A T A T C T C A G C T G A A A A C T T C C A G C A C A T T G G								Db
Qy	781	G G T G G A G G G C T G C C T C A C T T G G G T C C A G C T C C C C G C T C T G G C C A T T G G G C T G C								Qy
Db	1963	G G T G G A G G G C T G C C T C A C T T G G G T C C A G C T C C C C G C T C T G G C C A T T G G G C T G C								Db
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LOCUS		DEFINITION		Sequence 704 from patent US 6512094.		ACCESSION		ACCESSION		ACCESSION
VERSION		VERSION		AR278711		VERSION		AR278711		VERSION
KEYWORDS		KEYWORDS		GI:29712957		KEYWORDS		KEYWORDS		KEYWORDS

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REFERENCE	1	(bases 1 to 4034)	
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6620922-A 704 16-SEP-2003;		
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Qy	296	GGCCTCCCTACACCGGGAGAACGGGTTACCTCTAGCCCTGCAAGTCTGCACACT	355
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Qy	356	AGGTGCTAGGAGCAGCAGCTGTTCTGCCAAATACGGAGGGACACTGG	355
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Qy	476	GCTCTGCCGGCTCTGCCCTGCTGGGTGAGCCACCGCCACCGA	535
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Qy	536	GGCCAGGGGGTCCGGGGGGCATCTGCCATCCTGGATAGTGCT	595
Db	2423	GGCCAGGGGGTCCGGGGGGCATCTGCCATCCTGGATAGTGCT	2482

QY	1255 TGAAGTTATTTGTAGGGGAGAGTCCGTGAGGGCAACACAAAGAACCGTCCCTCA 1314	AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
Db	3143 TGAAGTTATTTGTAGGGGAGAGTCCGTGAGGGCAACACAAAGAACCGTCCCTCA 3202	JOURNAL	Patent: US 6759515-A 704 06-JUL-2004;
QY	1315 GCCCACAGCACTGTCTTGTGATCCACCCCTCTTACCTTTATCAGGATGTGCC 1374	FEATURES	Compositions and methods for the therapy and diagnosis of prostate cancer
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DEFINITION	Sequence 704 from patent US 6759515.	QY	776 ATGGGGTGGAGGGCTGCCTCACTGGTCCAGCTCCCGCTCTGGTAGGCCCCATGGG 835
ACCESSION	AR564090	Db	2663 ATTGGGGTGGAGGGCTGCCTCACTGGTCCAGCTCCCGCTCTGGTAGGCCCCATGGG 2722
VERSION	AR564090.1	QY	836 GCTGCCGGCTGGCCAGTTCTGTGCTGCCAACAGTAATGGGCTCTGTGCCAC 895
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ORGANISM	Unknown.		
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QY	956	CCCAGTCTCTAGGCTGCTGACTGGAGGCTTCCAAGGGTTTCAGTCAGTCTGACTTATA	1015	Db	3922	GCAATAATGTCGTCATTGCGGCTTCAAGGGGTTTCAGTCAGTCTGACTTATA	3981
QY	2843	CCCACTCTAGGCTGCTGACTGGAGGCTTCAAGGGGTTTCAGTCAGTCTGACTTATA	2902	QY	2095	AGAGTATAATGTTATGGTGACAAATTAAAGGCTTCTTATATGTTA	2143
QY	1016	CAGGGAGGCCAGAAGGGCTCATGCACTGGAGAATGC-GGGACTCTGCAGGTGATTACCA	1074	Db	3982	AGAGTATAATGTTATGGTGACAAATTAAAGGCTTCTTATATGTTA	4030
QY	2903	CAGGGAGGCCAGAAGGGCTCCATGCACTGGAGAATGCAGGTGATTACCA	2962	QY	1075	GGCTCAGGGTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGAG	1134
QY	2963	GGCTCAGGGTTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGAG	3022	Db	2035	GCAATAATGTCGTCATTGCGGATATTATACTGTAAGTGAGCAATC	2094
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QY	3023	CTGAATAACTCACTCACCTGGTTCCCATCTCTAAACCCCTAACCTGCACTTCGTT	3082	QY	2095	AGAGTATAATGTTATGGTGACAAATTAAAGGCTTCTTATATGTTA	2143
QY	1195	AATGTCAGCTCTGCATGGAGTTCTAGGATGAAACACTCCTCCATGGATTTGAAACA	1254	Db	3982	AGAGTATAATGTTATGGTGACAAATTAAAGGCTTCTTATATGTTA	4030
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QY	1255	TGAAAGTTATTGCTAGGGGAAGAGTCTGAGGGCAACACACACAGAACCCCTCA	1314	Db	2035	GCAATAATGTCGTCATTGCGGATATTATACTGTAAGTGAGCAATC	2094
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QY	1495	GGGTGGGGATCCCAACAAATCAGGCTCCCTGAGATACTGCTGGCATGGGCTGATCATG	1554	Db	2035	GCAATAATGTCGTCATTGCGGATTTGAAACAACACTCCTCCATGGATTTGAAACA	2094
QY	3382	GGGTGGGGATCCCAACAAATCAGGCTCCCTGAGATACTGCTGGCATGGGCTGATCATG	3441	QY	1075	GGCTCAGGGTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGAG	1134
QY	1555	CCAGAACTCTCTCTCTGGGGTCTGGGCCCCAAATGCCTAAACCCAGGACCTGGAA	1614	Db	2035	GCAATAATGTCGTCATTGCGGATTTGAAACAACACTCCTCCATGGATTTGAAACA	2094
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QY	3622	CAGCCTGGTCCCCCACTCCACTCCCTACTCTCTAGGACTGGGCTGATGAAGG	3681	QY	1075	GGCTCAGGGTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGAG	1134
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QY	3802	TGTCACATCTCAGCCCCAGACTATATCTGCTTGGGAATCTCACACAGAACTCAAG	3861	QY	1075	GGCTCAGGGTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAAGGGTTTGGAG	1134
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 11:26:32 ; Search time 6982.34 Seconds
(without alignments)
11682.581 Million cell updates/sec

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Perfect score: 2143

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Scoring table: GLRGONUGGT Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gbb1:*

9: gb_gbb2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
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LOCUS HSM804244 mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp666D0110 (from clone DKFZp666D0110).
ACCESSION AL832933
VERSION AL832933.1
KEYWORDS GI:21733520
HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2477)
Authors Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp666D0110) is available at the RZPD Deutsches RessourcenZentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: <http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp666D0110> Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>. Location/Qualifiers
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Db		Db	1321	AGGGAGGCCAGAGGGCTCATGCACTGGAAATGCAGGGACTCTGCAGGGATTACCCAG	1380
Query	Query Match 89.4%; Score 1916; DB 3; Length 2477; Best Local Similarity 99.9%; Pred. No. 0; Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	Qy	1076	GCTCAGGGTTAACAGCTAGCTCTCTAGTTGAGACACACACTAGAGAAGGGTTTGGAGC	1135
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DEFINITION						genomic survey sequence.	
ACCESSION	AY407706						
VERSION	AY407706.1						
KEYWORDS							
AUTHORS							
ORGANISM							
Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1	(bases 1 to 1626)					
Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,							
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,							
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,							
Adams, M.D. and Cargill, M.							
TITLE	JOURNAL						
Direct Submission							
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,							
Rockville, MD 20850, USA							
COMMENT							
This sequence was made by sequencing genomic exons and ordering							
them based on alignment.							
FEATURES	source						
Location/Qualifiers							
REFERENCE	1	.1626					
/organism="Homo sapiens"							
/mol_type="genomic DNA"							
/db_xref="taxon:9606"							
gene							
ORIGIN							
Query Match		32.9%	:	Score 704:	DB 9:	Length 1626:	
Best Local Similarity		100.0%	:	Pred. No. 0;			
Matches		704;	Conservative	0;	Mismatches	0;	
					Indels	0;	
					Gaps	0;	
Qy	58	GCCTTCGGATGGCAGCCTGGGGCTGTCTCAGCGATTCGGCACTCGGAGCAGTCTCTC	117	REFERENCE	1	AGENCOURT_10810630	MAPCL Homo sapiens
Db	923	GCCTTCGGATGGCAGCCTGGGGCTGTCTCAGCGATTCGGCACTCGGAGCAGTCTCTC	982	DEFINITION		MAPCL Homo sapiens	clone IMAGE:6722106 5',
Qy	118	TGGTCATGGACCGGCTGGTCAGCGATTCGGCACTCGGAGCAGTCTCTC	177	ACCESSION	CA489628	mRNA sequence.	
Db	983	TGGTCATGGACCGGCTGGTCAGCGATTCGGCACTCGGAGCAGTCTCTC	1042	VERSION	CA489628.1	EST.	
Qy	178	CAGCTTCCCTGTGGCTGCCACATGCCATGCCACAGTGCGCCGGTGGTGGACAG	237	KEYWORDS			
Db	1043	CAGCTTCCCTGTGGCTGCCACATGCCATGCCACAGTGCGCCGGTGGTGGACAG	1102	COMMENT			
Qy	238	CTTCAGCCCCCTCACCGGGTCACTCTCGCCCTACACACTGG	297	FEATURES	source		
Db	1103	CTTCAGCCCCCTCACCGGGTCACTCTCGCCCTACACACTGG	1162	Location/Qualifiers			
Qy	298	CCTCCCTCTACACCGGGAGAGCAGGTGTTCTGCCAATACCGAGGGACACTGGAG	357	1. .897			
Db	1163	CCTCCCTCTACACCGGGAGAGCAGGTGTTCTGCCAATACCGAGGGACACTGGAG	1222	/organism="Homo sapiens"			
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/db_xref="taxon:9606"							
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,							
hTERT-HME1, LNCap"							
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/clone_lib="MAPCL"							
note="Vector: PCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;							
Subtracted with brain, liver, lung, kidney and muscle.							
Directionally cloned. Priming method: oligo-dT. Average							
insert size: 1800 bp. Library amplification: 26,000 fold.							
Kristi A. Egland, James J. Vincent, Robert Strausberg,							
Bungkook Lee & Ira Pastan: Discovery of new breast							

Qy	1692 TCAAGGTCTCACIGCTT 1708	Db	194 ATAATTCAAATGCTGTACCCAGGTTAGGGTGTGAAGGAAGGTTAGGGGGCTT 253
Db	601 TCAAGGTCTCACACGGCTT 617	Qy	1693 CAGGTCTCAACGGCTTCCCTAACCTCTCTTGCCAGCCTGGTCCCCAC 1752
		Db	254 CAGGTCTCAACGGCTTCCCTAACACCCCTCTCTGGCCAGCTGGTCCCCAC 313
		Qy	1753 TTCCACTCCCTCTACTCTCTAGGACTGGCTGATGAAGGCAGTGCCTAAATTCCCC 1812
		Db	314 TTCCACTCCCTCTACTCTCTAGGACTGGCTGATGAAGGCAGTGCCTAAATTCCCC 373
RESULT 5	CB048223	Qy	1813 CTACCCCCACTTCCCTACCCCAACTTCCCACCCAGCTCCACACCCGTGGAG 1872
LOCUS	CB048223	Db	374 CTACCCCCACTTCCCTACCCCAACTTCCCACCCAGCTCCACACCCGTGGAG 433
DEFINITION	NISC_gj03e11.y1 NCI_CGAP_Pr28	Qy	1873 CTACTGCAGGACCAAGCACAAGTGCCTTGTCCAAAGCCCTTGCCATCTCAGCCCC 1932
ACCESSION	5' mRNA sequence.	Db	434 CTACTGCAGGACCAAGCACAAGTGCCTTGTCCAAAGCCCTTGCCATCTCAGCCCC 493
VERSION	CB048223	Qy	1933 AGAGTATATCTGCTGCTGGGAATCTCACACAGAACTCAGAGCACCCCTGCCTGAGC 1992
KEYWORDS	EST.	Db	494 AGAGTATATCTGCTGCTGGGAATCTCACACAGAACTCAGAGCACCCCTGCCTGAGC 553
SOURCE	Homo sapiens (human)	Qy	1993 TAAGGGAGGTCTTATCTCTCAGGGGGTTAAGTGCCTTGCAATAATGTCGTCTTAT 2052
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	Db	554 TAAGGGAGGTCTTATCTCTCAGGGGGTTAAGTGCCTTGCAATAATGTCGTCTTAT 613
REFERENCE	1 (bases 1 to 651)	Qy	2053 TT 2054
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	Db	614 TT 615
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov		
JOURNAL	CDNA Library Preparation: DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: info@image.llnl.gov		
Plate: LILAB006	row: J column: 21		
seq primer: M13RP1 reverse primer (ABI).	Location/Qualifiers		
FEATURES	source		
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	/clone="IMAGE:3270644"		
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	/dev_stage="adult"		
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	/note="Organ: prostate; Vector: pTT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."		
ORIGIN			
	Query Match 28.1%; Score 602; DB 6; Length 651; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 602; Conservative 0; Indels 0; Gaps 0;		
Qy	1453 TCCATGTGCTAGCTTCTGCTGTTGGTCTAATATTGGTAGGGGGGGATCCCCAAC 1512	FEATURES	source
Db	14 TCCATGTGCTAGCTTCTGCTGTTGGTCTAATATTGGTAGGGGGGGATCCCCAAC 73		
Qy	1513 AATCAGGTCCCTGAGATAGCTGGCATGGCTGATCATGGCCAGAATCTTCTCTCT 1572		
Db	74 AATCAGGTCCCTGAGATAGCTGGCATGGCTGATCATGGCCAGAATCTTCTCTCT 133		
Qy	1573 GGGGTCTGCCAAATGCCAACCCAGGACCTGGAAATTCTACTCATCCCAAATG 1632		
Db	134 GGGGTCTGCCAAATGCCAACCCAGGACCTGGAAATTCTACTCATCCCAAATG 193		
Qy	1633 ATAATTCCAATGCTGTACCCAAAGGTTAGGGTGTGAAGGAAGGTTAGGGGGCTT 1692		
ORIGIN			
	Query Match 28.0%; Score 601; DB 7; Length 722; Best Local Similarity 99.9%; Pred. No. 1.9e-313; Mismatches 721; Conservative 0; Indels 1; Gaps 1;		

QY 751 ACTCAGCGTAGAAACTTCCAGCACATTGGGTGAGGGCCCTGCTCACTGGGCCAGC 810
 1 ACTCAGCGTAGAAACTTCCAGCACATTGGGTGAGGGCCCTGCTCACTGGGCCAGC 60
 Db 811 TCCCCGCTCTGTAGCCCCATGGGGCTGCCGGGCTGGCCAGTTCTGTGCTGCCA 870
 QY 61 TCCCCGCTCTGTAGCCCCATGGGGCTGCCGGGCTGGCCAGTTCTGTGCTGCCA 120
 Db 871 AAGTAATGTGGCTCTCTGTCACCCCTGTGCTGAGGTGGCTAGCTGACAGCTGG 120
 QY 121 AAGTAATGTGGCTCTCTGTCACCCCTGTGCTGAGGTGGCTAGCTGACAGCTGG 930
 Db 931 GCTGGGGCTCCCTCTCTCCCAGTCTAGGGCTGCCGTACTGGAGGCCCTCC 180
 QY 181 GCTGGGGCTCCCTCTCTCCCAGTCTAGGGCTGCCGTACTGGAGGCCCTCC 990
 Db 991 AAGGGGTTTCAGTCTGGACTTACAGGGAGGCCAGAAGGCTCCATGCACTGGAATGC 240
 QY 241 AAGGGGTTTCAGTCTGGACTTACAGGGAGGCCAGAAGGCTCCATGCACTGGAATGC 300
 Db 301 GGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCTAGTGGAC 360
 QY 1110 ACACCTAGAGAAGGGTTTGGGAGTAACTCAGTCACCTGGTTCCATCTCA 1169
 Db 361 ACACCTAGAGAAGGGTTTGGGAGTGAATAACTCAGTCACCTGGTTCCATCTCA 420
 QY 1170 ACCCCCTAACCTGCAGCTCGTTAATGTAGCTCTGATGGAGTTCTAGGATGAA 1229
 Db 421 AGCCCTTAACCTGCAGCTCGTTAATGTAGCTCTGATGGAGTTCTAGGATGAA 480
 QY 1230 CACTCTCCATGGGATTGTGACATATGAAGCTATTGTAGGGAGAGTCTGGAGGGC 1289
 Db 481 CACTCTCCATGGGATTGTGACATATGAAGCTATTGTAGGGAGAGTCTGGAGGGC 540
 QY 1290 AACACACAAGAACCGGTCCTAACCCACAGGACTGTCTTTGTGATCCACCCCCC 1349
 Db 541 AACACACAAGAACCGGTCCTAACCCACAGGACTGTCTTTGTGATCCACCCCCC 600
 QY 1350 TCTTACCTTATCAGGATGTGGCTCTGTGATCCATCACAGAGACAGG 1409
 Db 601 TCTTACCTTATCAGGATGTGGCTCTGTGATCCACAGAGACAGG 660
 QY 1410 CATTAAATATTAACTTATTAAACAAGTAGAAGGAAATCCATTGCTAGTTTC 1469
 Db 661 CATTAAATATTAACTTATTAAACAAGTAGAAGGAAATCCATTGCTAGTTTC 720
 QY 1470 TG 1471
 Db 721 TG 722

FEATURES

source

COMMENT

Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-28, >AT rich#Low_complexity
 Seq primer: M13 FORWARD
 POLYA=Yes.

LOCATIONS

Location/Qualifiers

1. .670

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EC1-ady-f-04-0-UI"
 /tissue_type="Lung"
 /dev_stage="Adult and Fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EC1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified Polylinker; Site_1: ECO R; Site_2: Not I;
 UI-CF-EC1 is a normalized cDNA library containing the
 following tissue(s): Normal lung from adult and from fetal
 day 64, day 87, week 19 and week 42. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an ECO R
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 (AT)18 tail. The sequence tag for this library is
 AAGTGCCTAC.
 TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
 and 380-383
 TAG LIB=UI-CF-EC1
 TAG_SEQ=AAGTGCCTAC"

ORIGIN

Query Match
 Best Local Similarity 27.7%; Score 593; DB 5; Length 670;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1500 GGGGATCCCCAACATCAGGTCCTGTGAGATAGCTGGTCATTGGGTGATCATGCCAGA 1559
 Db 661 GGGGATCCCCAACATCAGGTCCTGTGAGATAGCTGGTCATTGGGTGATCATGCCAGA 602
 QY 1560 ATCTTCTCTCTGGGTCTGGCCCCAACATGCCTAACCCAGGACCTGGAAATTCTA 1619
 Db 601 ATCTTCTCTCTGGGTCTGGCCCCAACATGCCTAACCCAGGACCTGGAAATTCTA 542
 QY 1620 CTCATCCAAATGATAATTCAAATGCTGTACCCAGGTAGGGTGTGAGGAAGTA 1679
 Db 541 CTCATCCAAATGATAATTCAAATGCTGTACCCAGGTAGGGTGTGAGGAAGTA 482
 QY 1680 GAGGGGGGACTCAGGCTCAACGGCTTCCCTAACCCCTCTCTCTGGCCAGCC 1739
 Db 481 GAGGGGGGCTCAGGCTCAACGGCTTCCCTAACCCCTCTCTGGCCAGCC 422
 QY 1740 TGGTCCCCCACTCCACTCCCTACTCTCTTAGGACTGGGTGATGAGGACTG 1799
 Db 421 TGGTCCCCCACTCCACTCCCTACTCTCTTAGGACTGGGTGATGAGGACTG 362

RESULTS

7
 BU689021/c
 DEFINITION UT-CF-EC1-ady-f-04-0-UI .s1 UI-CF-EC1 Homo sapiens EST 07-OCT-2002
 ACCESSION BU689021
 VERSION BU689021.1 GI:23546376
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 670)
 AUTHORS Bonaldo, M. F., Lennon, G. and Soares, M. B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9); 791-806 (1996)
 MEDLINE 9704477
 PUBMED 8889548

Qy 1800 CCCAAATTCCCCCTACCCCAACTTCCCTACCCCAACTTCCCCAACCTTCCCCACCCAGCTCCACA 1859 ORIGIN Technologies."

Db 361 CCCAAATTCCCCCTACCCCAACTTCCCTACCCCAACTTCCCCACCCAGCTCCACA 302

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Db 301 ACCCTGTTGGAGCTACTGGAGGACAGAACAGGAGCTTCCAAAGCCTTGTC 242

Qy 1920 CATCTCAGCCCCAGAGTATCTGTGCTGGGAATCTCACAGAACTCAGGAC 1979

Db 241 CATCTCAGCCCCAGAGTATCTGTGCTGGGAATCTCACAGAACTCAGGAC 182

Qy 1980 CCCCTGCCTAGCTAAGGGAGGTCTATCTCTAGGGGTTAAGTGCCTTGCAAT 2039

Db 181 CCCCTGCCTAGCTAAGGGAGGTCTATCTCTAGGGGTTAAGTGCCTTGCAAT 122

Qy 2040 AATGTCGCTTATTATTTAGCGGGGTAAATTTATCTGTAAAGCAATCAGACT 2099

Db 121 AATGTCGCTTATTATTTAGCGGGGTAAATTTATCTGTAAAGCAATCAGACT 62

Qy 2100 ATAATGTTATGGTGACAAATTAAAGGTTCTTATATGTTA 2143

Db 61 ATAATGTTATGGTGACAAATTAAAGGTTCTTATATGTTA 18

RESULT 8

BQ950805 BQ950805 959 bp mRNA linear EST 21-AUG-2002

LOCUS BQ950805 8842232 Lupski_sciaitic_nerve Homo sapiens CDNA clone

DEFINITION AGENCOURT 8842232 Lupski_sciaitic_nerve Homo sapiens CDNA clone

IMAGE:6204253 5', mRNA sequence.

ACCESSION BQ950805

VERSION BQ950805.1 GI:22366283

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 599)

AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM13625 row: d column: 14

High quality sequence start: 2

High quality sequence stop: 490.

FEATURES Source

1. .959

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6204253"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

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/note="Vector: PCMV-SPORT (Life Technologies); Site_1: NotI; Site_2: SalI; CDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGGCTCCG-3', and 5'-GACTAGTCTAGATCGCGAGCGGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life

RESULT 9

BB867241 BB867241 718 bp mRNA linear EST 20-OCT-2000

LOCUS BB867241 601442309F1 NIH_MGC_65 Homo sapiens CDNA clone IMAGE:3846411 5', mRNA sequence.

DEFINITION BE867241

ACCESSION BE867241.1 GI:10316017

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 718)

AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Db 492 GCTCCTAGTTGAGACACACTAGAGAAGGGT"rrGGAGCTGAATAACTCAGTCAC 551
 Qy 1154 TGTTTCCCATCTCTAAGCCCTTAACCTGCAGCTCGTTAATGTAGCTCTGCATGGG 1213
 Db 552 TGTTTCCCATCTCTAAGCCCTTAACCTGCAGCTCGTTAATGTAGCTCTGCATGGG 611
 Qy 1214 AGTTCTAGGATGAAACACTCCTCATGGATTGAACATATGAAGTTATGGGG 1273
 Db 612 AGTTCTAGGATGAAACACTCCTCATGGATTGAACATATGAAGTTAGGGG 671
 Qy 1274 AAGAGTCTGAGGGCACACCAAGAACAGGATTTGAACATATGAAGTTATGGGG 1333
 Db 672 AAGAGTCTGAGGGCACACCAAGAACAGGATTTGAACATATGAAGTTAGGGG 731
 Qy 1334 TGCTGATCCACCCCTTACCTTATCAGGATGTGCC 1374
 Db 732 TGCTGATCCACCCCTTACCTTATCAGGATGTGCC 772

RESULT 11
 CN373214 LOCUS CN373214 581 bp mRNA linear EST 16-MAY-2004
 DEFINITION 1700532189001 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN373214
 VERSION CN373214.1 GI:47373148
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
 TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 581 Std Error: 0.00.

FEATURES source
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 /db_xref="taxon:9606"
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 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 8.3e-274; Mismatches 0; Indels 0; Gaps 0;
 Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 CCTGGTTCCCATCTCTAAGCCCTTAACCTGCAGCTCGTTAATGTAGCTCTGCATG 1211
 Db 39 CCTGGTTCCCATCTCTAAGCCCTTAACCTGCAGCTCGTTAATGTAGCTCTGCATG 98
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 Db 99 GGAGTTCTAGGATGAAACACTCCTCATGGATTGAACATATGAAGTTATGGGG 158
 Qy 1272 GGAGAGTCTGAGGGCACACACAGAACCCAGGTCCCTCAGCCACAGCACTGTCT 1331

Db 159 GGAAGAGTCTGAGGGCACACACAGAACCCAGGTCCCTCAGCCACAGCACTGTCT 218
 Qy 1332 TTTGTGATCCACCCCTCTACCTTATCAGGATGTGGCTGTTGTTCTCTG 1391
 Db 219 TTTGTGATCCACCCCTCTACCTTATCAGGATGTGGCTGTTGTTCTCTG 278
 Qy 1392 CCATCACAGAGACAGGAATTAACTTAACTTAACTAACAAGTAGAGGA 1451
 Db 279 CCATCACAGAGACAGGAATTAACTTAACTTAACTAACAAGTAGAGGA 338
 Qy 1452 ATCCATTGCTAGCTTCTGTGTTGGTCTAATTGGGTAGGGTAGGGATCCCA 1511
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 Qy 1512 CAATCAGGTTCCCTGAGATAGCTGGTCTATGGGTGATCATGCCAGATCTCTCC 1571
 Db 399 CAATCAGGTTCCCTGAGATAGCTGGTCTATGGGTGATCATGCCAGATCTCTCC 458
 Qy 1572 TGGGGTCTGGCCCCCAAATGCCTAACCCAGGACCTGGAAATTCTACTCATCCCAAT 1631
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RESULT 12
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 DEFINITION 602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5', mRNA sequence.
 ACCESSION BG469586
 VERSION BG469586.1 GI:13401861
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LLM1460 row: k column: 05
 High Quality sequence stop: 587.
 Location/Qualifiers 1. .589
 /organism="Homo sapiens"
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 /clone="IMAGE:4661500"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_15"
 /note="Oligo dT primed, directionally cloned into ECORI/XbaI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Tissue Procurement: Dr. Mark Watson	
CDNA Library Preparation: Rubin Laboratory	
DNA sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	
http://image.llnl.gov	
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High quality sequence stop: 485.	
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/lab_host="DH10B (phage-resistant)"	
/clone_lib="NIH MGC_113"	
/note="Organ: spleen; Vector: pOTB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN	
Query Match 22.1%; Score 474; DB 5; Length 1060;	
Best Local Similarity 100.0%; Pred. No. 1.6e-244;	
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 352 CTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTCCTGCCAGGCCCTAAGCCTG 411	
Db 1 CTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTCCTGCCAGGCCCTAAGCCTG 60	
Qy 412 GAGGCTCCCTCCCTAATGGACACGTGGTGTGGAGGCAGTGGCTGCTCCACCTCAC 471	
Db 61 GAGCTCCCTCCCTAATGGACACGTGGCTGCTGGAGGCAGTGGCTGCTCCACCTCAC 120	
Qy 472 CCGGCGCTCTGGGGCTCTGCATGATGCTCCGTACGTGGTGGGGAGGCCA 531	
Db 121 CCGGCGCTCTGGGGCTCTGCATGATGCTCCGTACGTGGTGGGGAGGCCA 180	
Qy 532 CCGGAGGCCAGGGTGGTCCGGGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTG 591	
Db 181 CCGGAGGCCAGGGTGGTCCGGGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTG 240	
ORIGIN	
Query Match 21.4%; Score 459; DB 5; Length 515;	
Best Local Similarity 100.0%; Pred. No. 2.1e-236;	
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 652 AGTCTGTCACTGCCTATATGGTGTCTGCCGCCAGGTGGCTTATGGCTTCATGTCCAGCTCAGCC 651	
Db 241 CCTTCTCTGCTCCCAGGTGGCCCATCCCTGTTATGGCTTCATGTCCAGCTCAGCC 300	
Qy 301 AGTCTGTCACTGCCTATATGGTGTCTGCCGCCAGGTGGCTTATGGCTTCATGTCCAGCTCAGCC 711	
Db 34 TAACCCAGGACCTTGAATTCCTACTCCAAATGATAATTCCAAATGCTGGTACCCA 360	
Qy 712 CTACACAGGTAGTATTGACAAGAGCGACTTGCCCAAATACTCAGCGTAGAAACTCCA 771	
Db 361 CTACACAGGTAGTATTGACAAGAGCGACTTGCCCAAATACTCAGCGTAGAAACTCCA 420	
Qy 772 GCACATGGGGGGAGGCCCTGCCTCACTGGTCCCAGCTCCCCGCTCTGTAA 825	
Db 421 GCACATGGGGGGAGGCCCTGCCTCACTGGTCCCAGCTCCCCGCTCTGTAA 474	
ORIGIN	
Query Match 21.4%; Score 459; DB 5; Length 515;	
Best Local Similarity 100.0%; Pred. No. 2.1e-236;	
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1596 TAACCCAGGACCTTGAATTCCTACTCCAAATGATAATTCCAAATGCTGGTACCCA 1655	
Db 34 TAACCCAGGACCTTGAATTCCTACTCCAAATGATAATTCCAAATGCTGGTACCCA 93	
Qy 1656 AGGTAGGGTGTGAAGGAAGGTAGAGGGTAGGGTGGGCTTCAGGTCTCAACGGCTTCCCTAAC 1715	
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Qy 1716 CACCCCTCTCTGGCCAGGCTGGTCCCCACTTCACCTCCCTACTCTCTCT 1775	
Db 154 CACCCCTCTCTGGCCAGGCTGGTCCCCACTTCACCTCCCTACTCTCTCT 213	
Qy 1776 AGGACTGGGCTGATGAAGGCCACTGCCCAAATTCCCTAACCTTCCCTACCC 1835	
Db 214 AGGACTGGGCTGATGAAGGCCACTGCCCAAATTCCCTAACCTTCCCTACCC 273	
Qy 1836 CCACTTCCCCACAGCTCCACAAACCTGTTGGAGCTACTGCAGGACAGACAA 1895	
Db 274 CCACTTCCCCACAGCTCCACAAACCTGTTGGAGCTACTGCAGGACAGACAA 333	
Qy 1896 AGTGGCGTTTCCAAAGCCTTGTCCATCTAGCCCCAGAGTATATCTGTGCTGGGAA 1955	
FEATURES	
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AUTHORS	
COMMENT	
TITLE JOURNAL	
Human Unigeneset - RZPD3	
Unpublished (2003)	
Contact: Ina Rolfs	
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany	
RZPD; IMAGP998P04693.	
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;	
Human UnigeneSet - RZPD3 (RZPDLIB No.972)	
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972	
Contact: Ina Rolfs	
RZPDLIB Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
Heubnerweg 6, D-14059 Berlin, Germany	
Tel: +49 30 32639 101	
Fax: +49 30 32639 111	
www.rzpd.de	
This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.	
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